```
1                                                   31
TCG ACT ATG AAT GCA GAT ACA GCT CCA ACA TCT CCT TGT CCT TCC ATA TCT TCC CAG AAC
ser thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asn

61                                                  91
TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC AGC ATG TTC GAT CGG ACT TCC
ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser

                                                        Cadherin
121                                                 151      xx EC motif xx|
AGA GTA CCC GCC AGC AGC ACT TCC TCA CCG GGG CTC CTC TTC ACA GAA CTG GCT GCT GCC
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala

181                                                 211
CTG GAT GCC GAA GGG GAA GGA ATC AGC GAA GTA CAA AGG AAA GCT GTC AGT GCA ATT CAC
leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his

241                                                 271
AGC CTG CTA AGT TCT GAC GAC CTG GAC CCA CGC TGT GTC AAA CCA GAG GTG AAG GTC AAA
ser leu leu ser ser asp asp leu asp pro arg cys val lys pro glu val lys val lys

301                                                 331
ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA GAG CTC TGT
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

361                                                 391
GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC TCG GAT GAA GAA CAA GAA
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

421                                                 451
GGA GCC AGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu

481                                                 511
AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

541                                                 571
GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

601                                                 631
CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA
leu ile arg lys trp ile ala asp leu pro ser thr gln leu asn arg ile leu asp leu

661                                                 691
TTT TTT ATT TAT TTT TTA ATT TTT GAT GAT AAT TTA AAA TAT ATT GAT AAA TTT ATT
leu phe ile tyr phe leu ile phe asp asp asn leu lys tyr ile asp lys phe ile

721                                                 751
ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG GAA GAG GCT TTG CTG CGT
thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg

781                                                 811
GGG GAA GGG GCT AGA GGG GAC ATG ATG CCC CAC GAT TCT CTA GGC AAC GAC TGA TTT CTA
```

FIG. 1 (1 of 5)

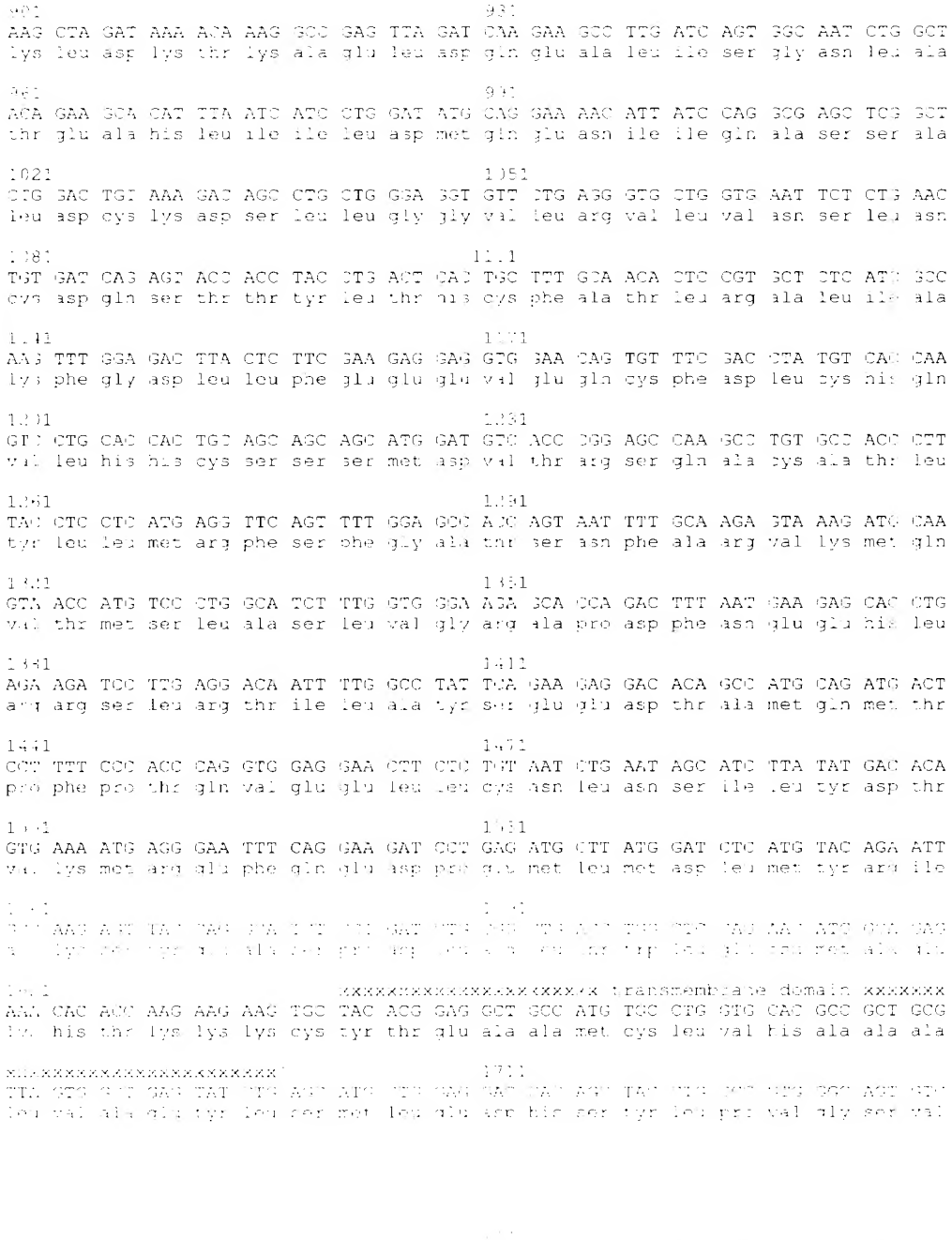


FIG. 1 (2 of 5)

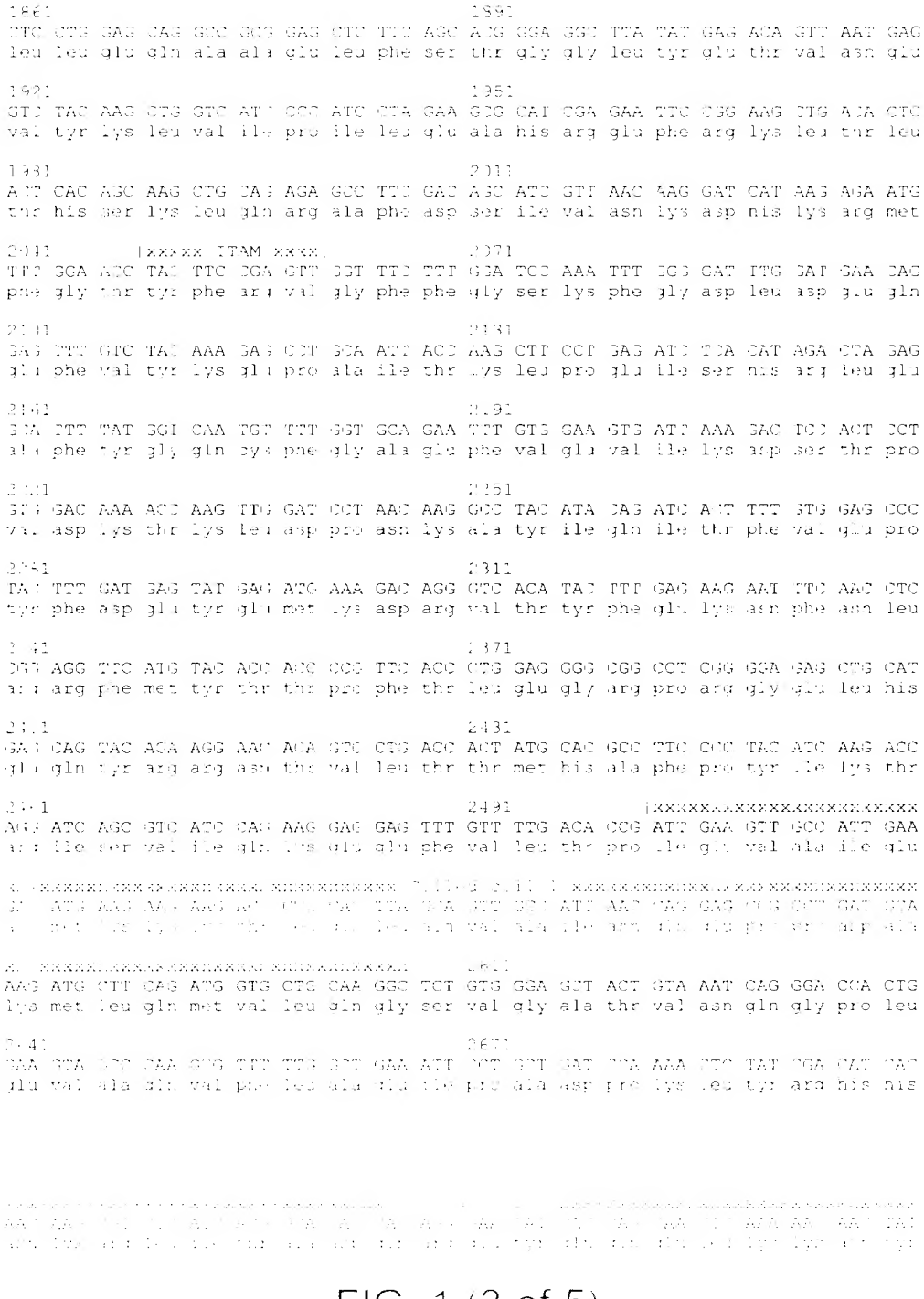


FIG. 1 (3 of 5)

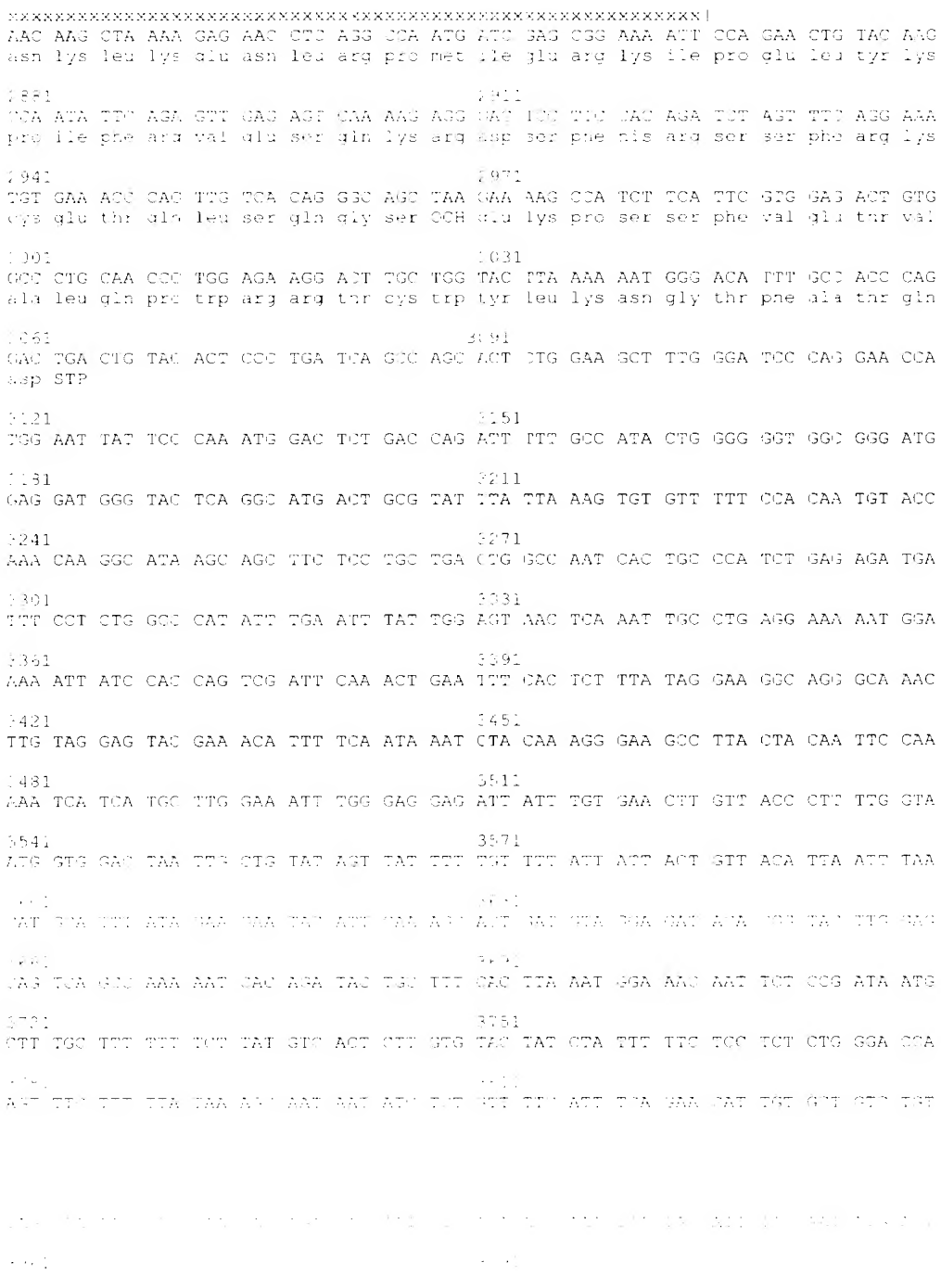


FIG. 1 (4 of 5)

4021
AAC TCG

FIG. 1 (5 of 5)

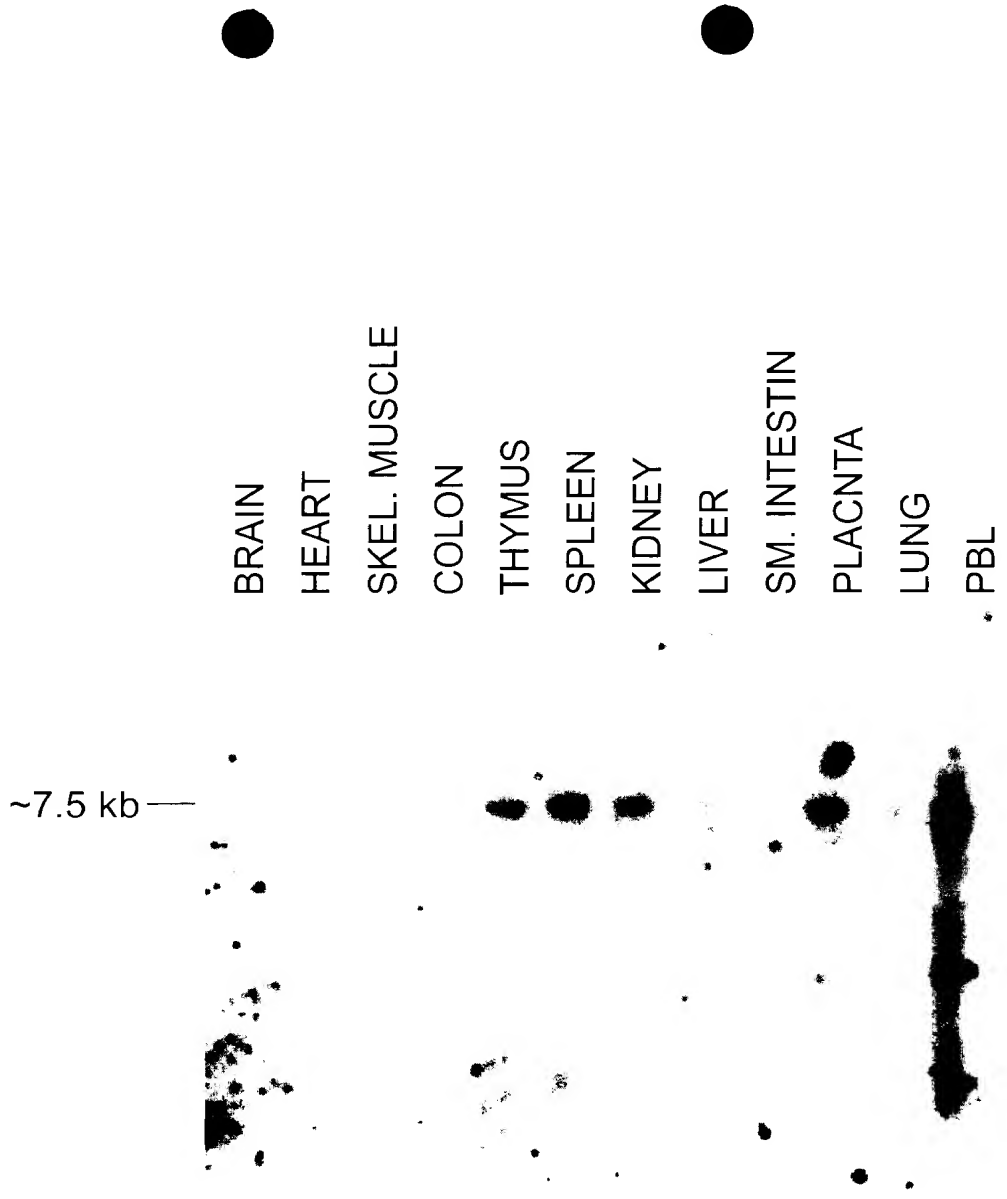

BRAIN
HEART
SKEL. MUSCLE
COLON
THYMUS
SPLEEN
KIDNEY
LIVER
SM. INTESTIN
PLACNTA
LUNG
PBL
~7.5 kb

FIG. 2A

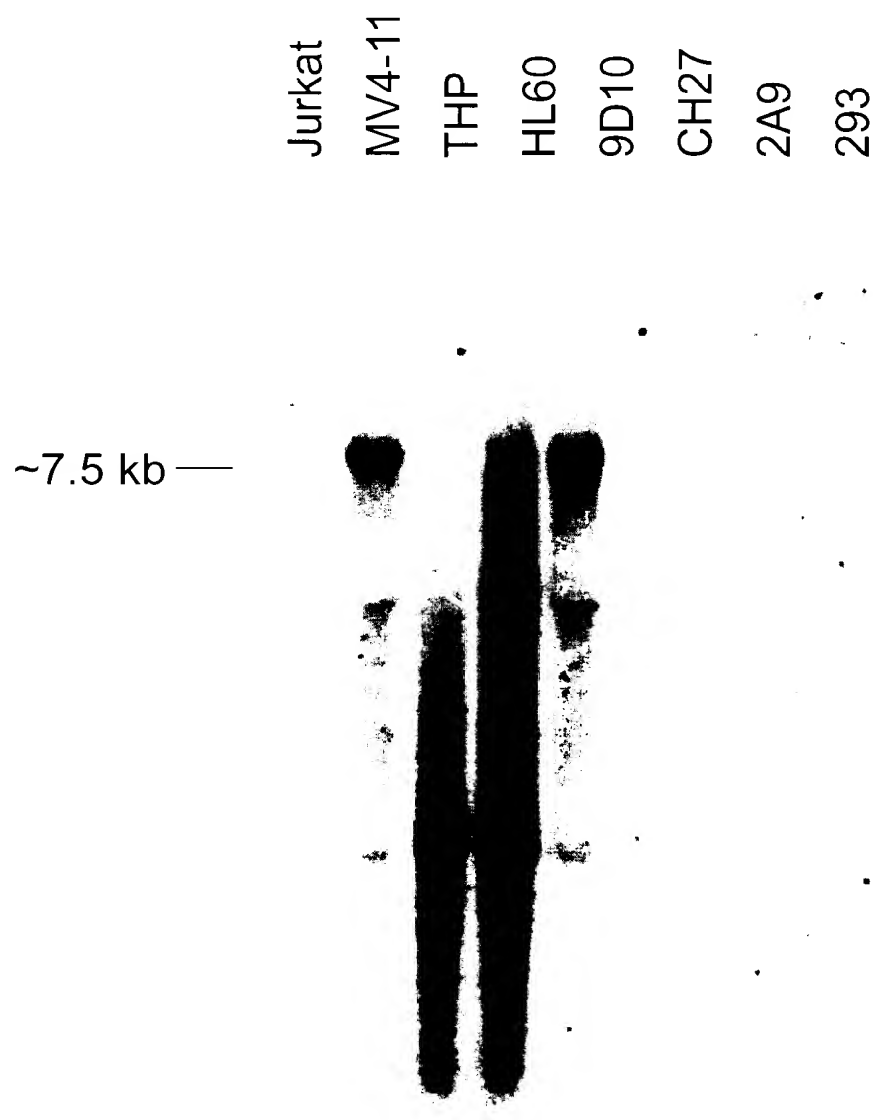


FIG. 2B

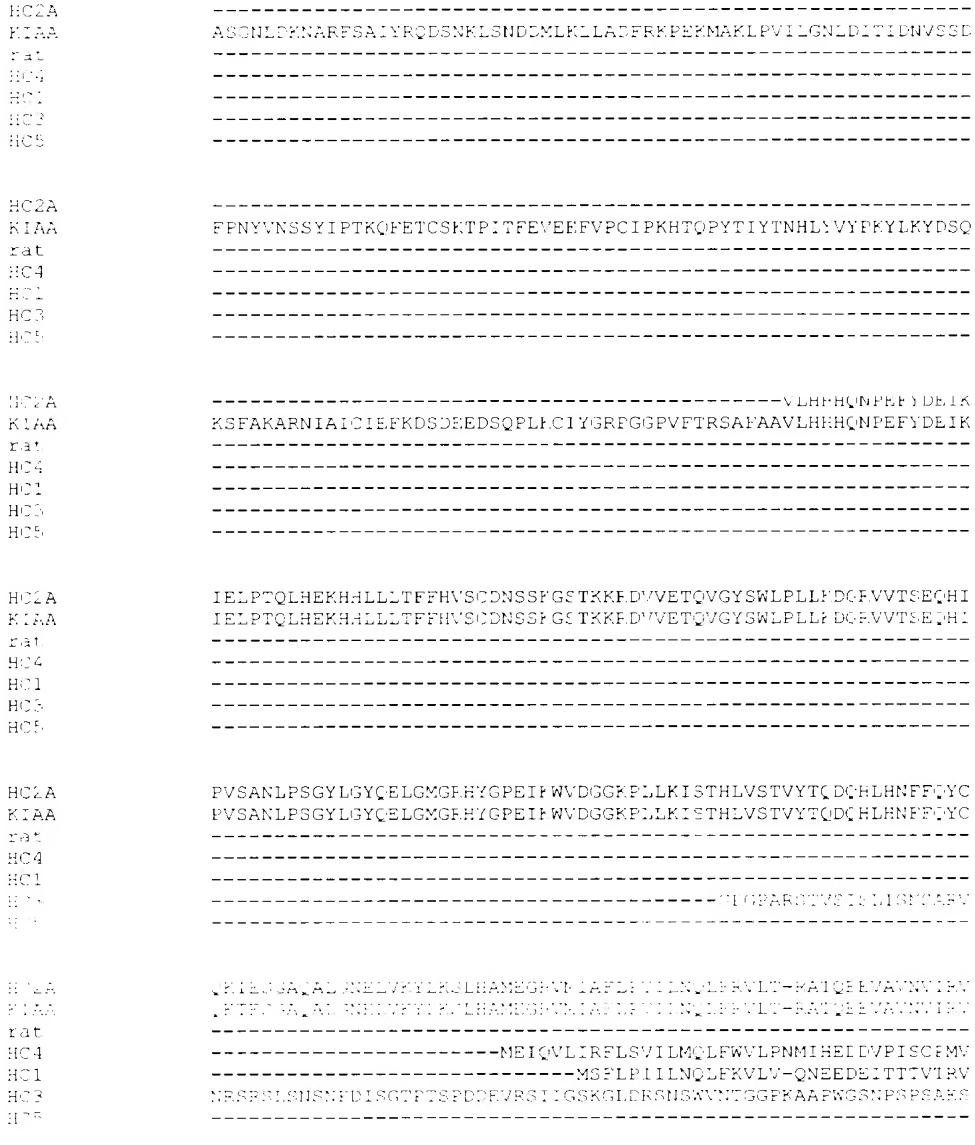


FIG. 3A (1 of 5)

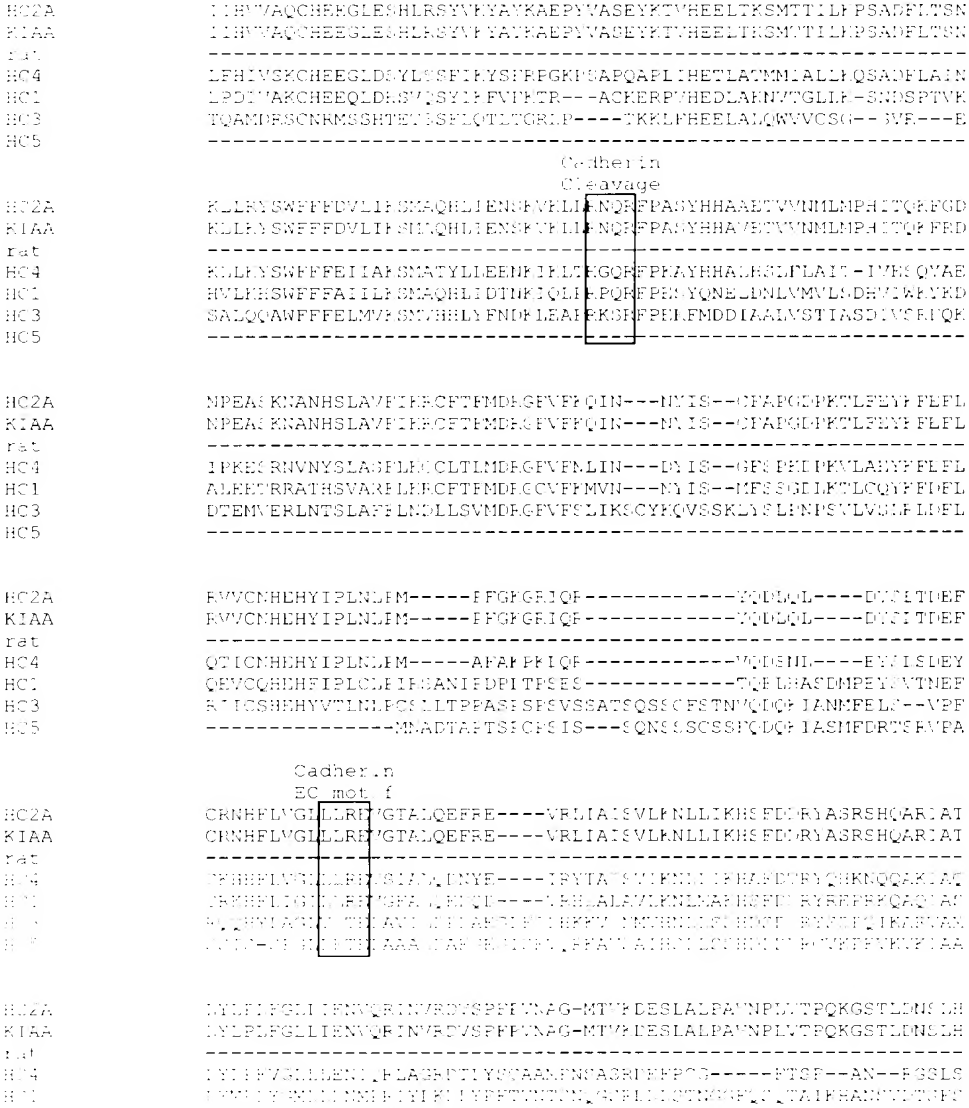


FIG. 3A (2 of 5)

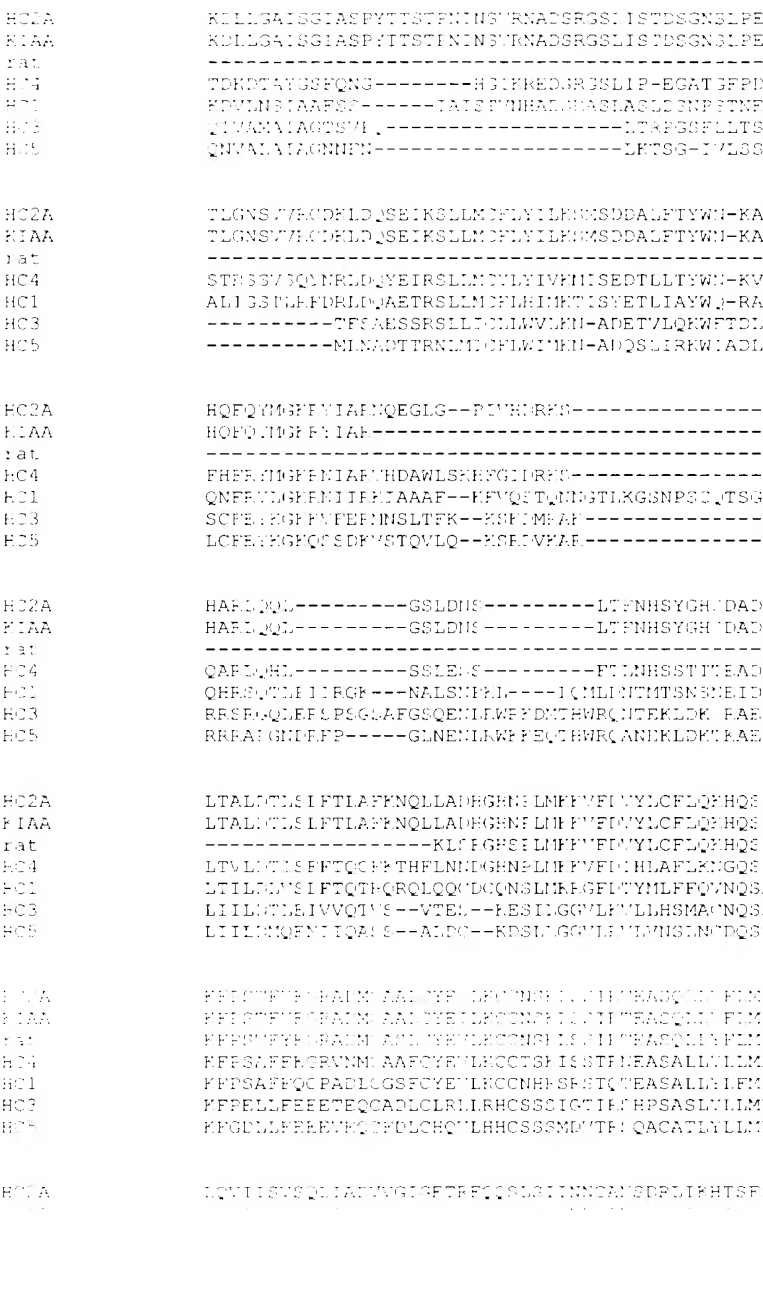


FIG. 3A (3 of 5)

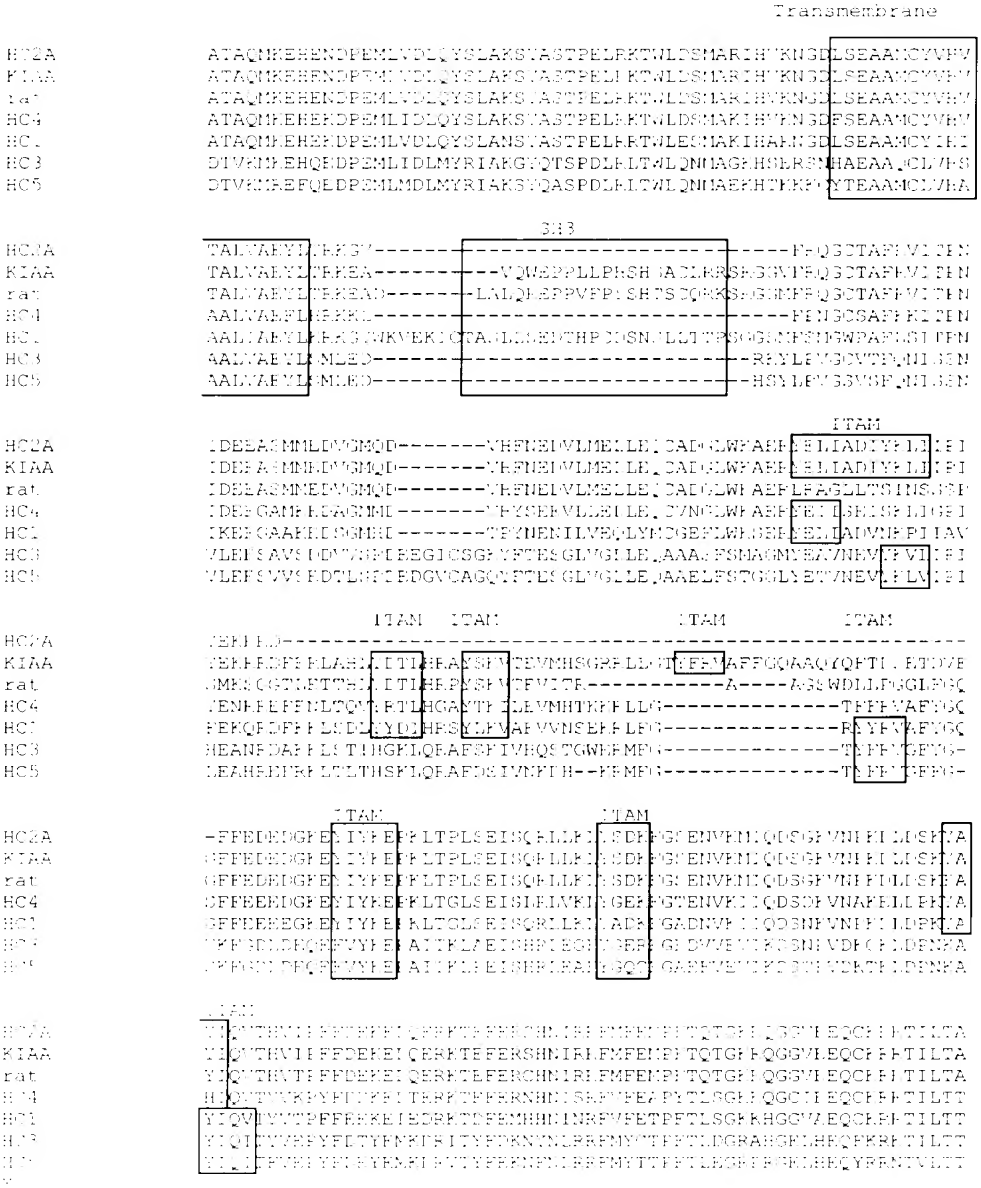


FIG. 3A (4 of 5)

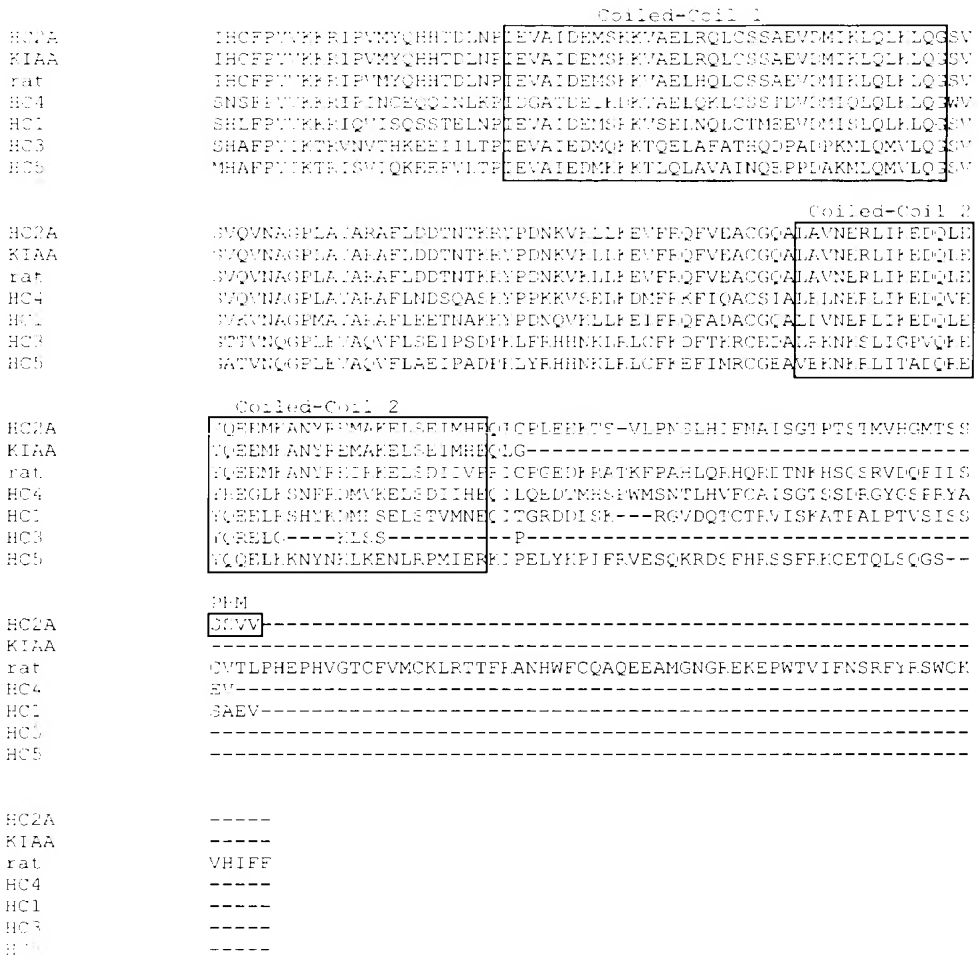


FIG. 3A (5 of 5)

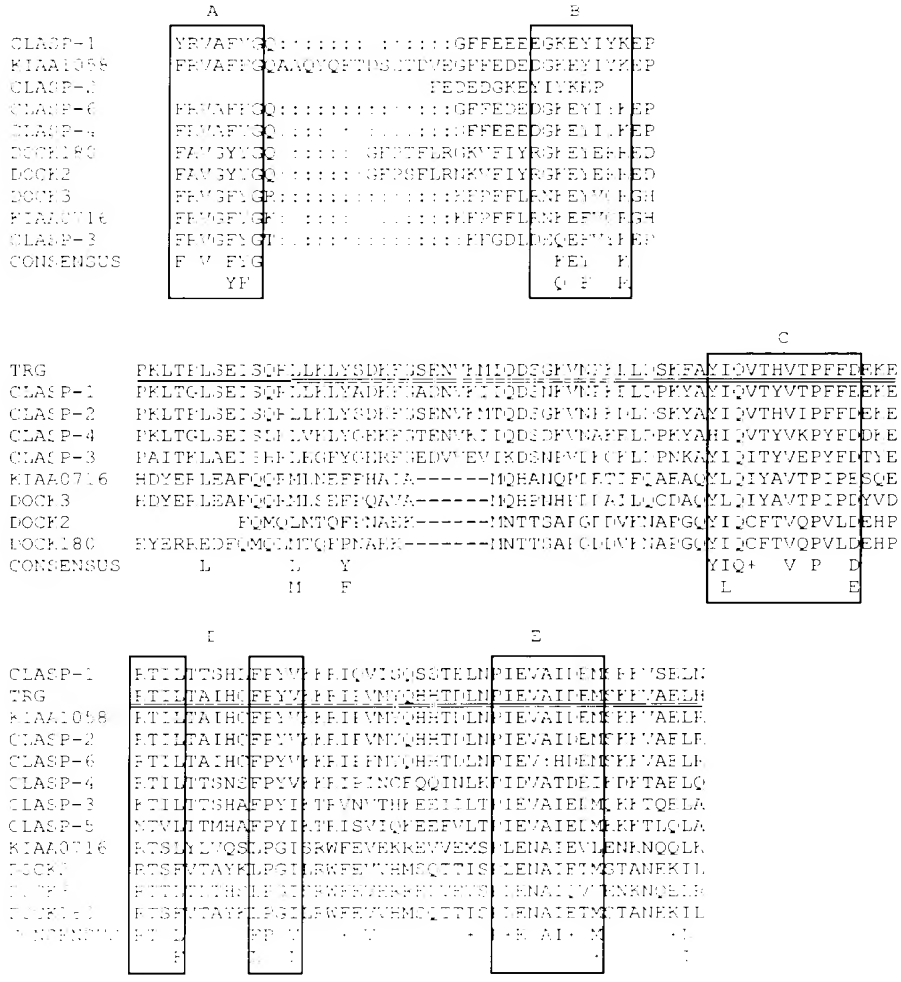
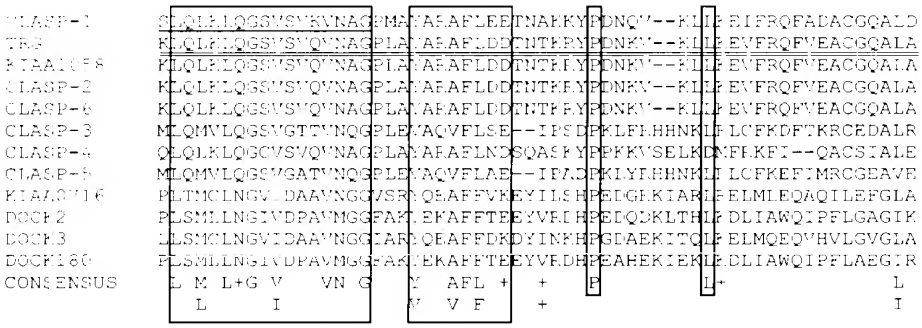

A
B
C
D
E
TRG
CLASP-1
CLASP-2
CLASP-4
CLASP-3
KIAA0716
DOCK3
DOCK2
DOCK180
CONSENSUS

FIG. 3B (1 of 2)



DOCK2=KIAA0209
DOCK3=KIAA0299
CLASP2variant=KIAA1058

FIG. 3B (2 of 2)

FIG. 4A (1 of 7)

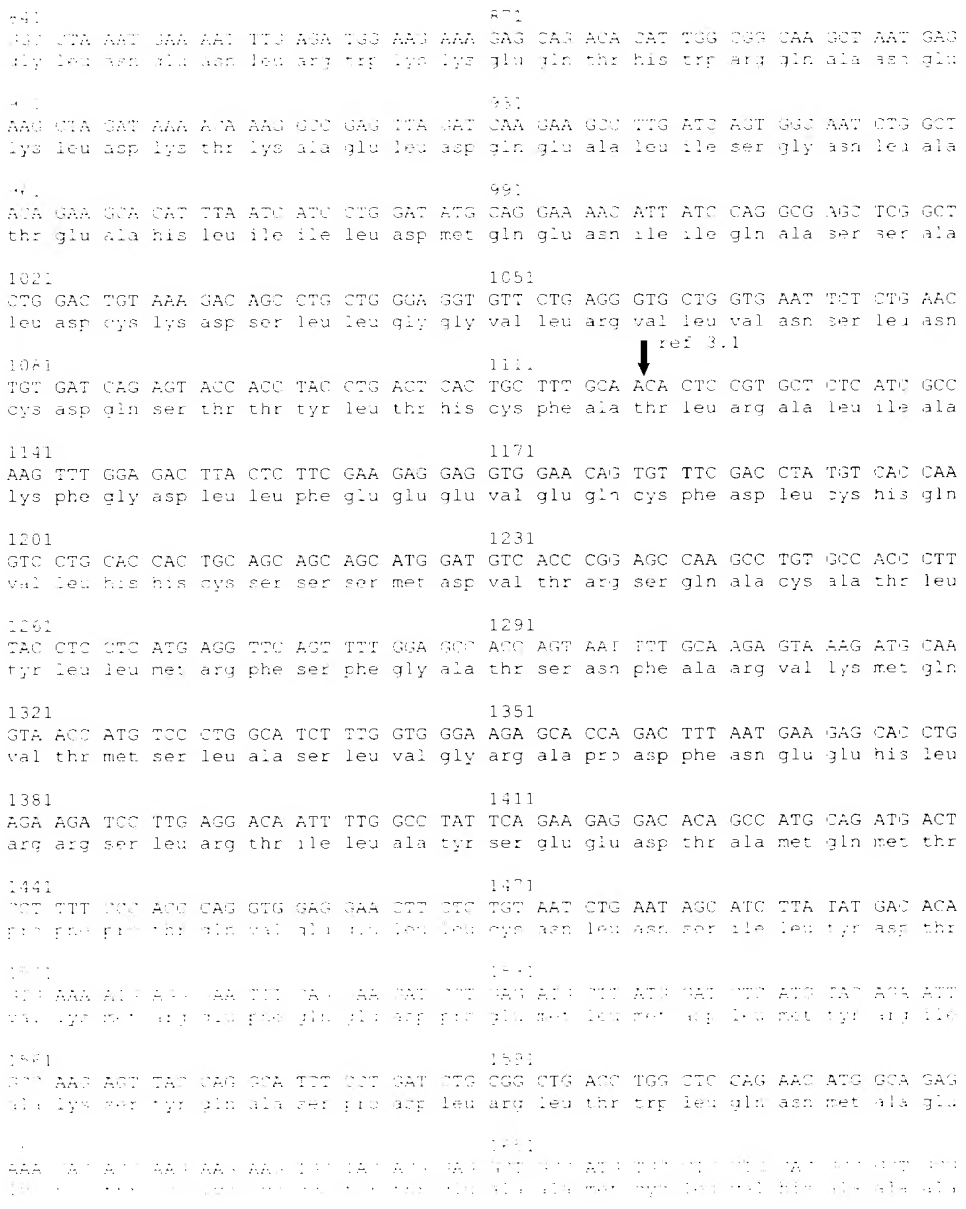


FIG. 4A (2 of 7)

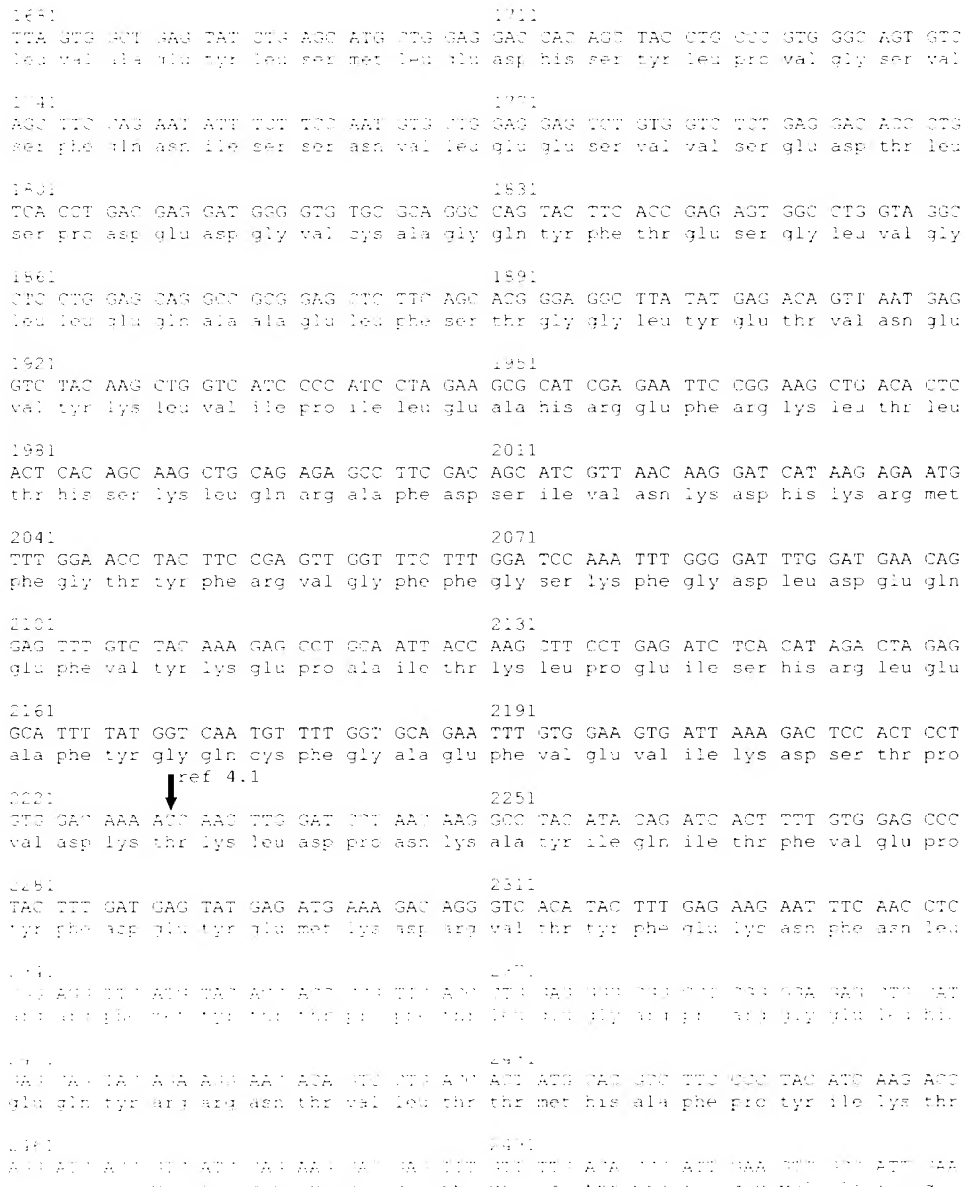

1681
1711
TTA GTG GCT GAG TAT CTG AGC ATG TTG GAG GAC CAC AGC TAC CTG CCC GTG GGC AGT GTC
leu val ala glu tyr leu ser met leu glu asp his ser tyr leu pro val gly ser val
1741
1771
AGC TTC CAG AAC ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG GTC TCT GAG GAC ACC CTG
ser phe gln asn ile ser ser asn val leu glu glu ser val val ser glu asp thr leu
1801
1831
TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC GAG AGT GGC CTG GTA GGC
ser pro asp glu asp gly val cys ala gly gln tyr phe thr glu ser gly leu val gly
1861
1891
CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG
leu leu glu gln ala ala glu leu phe ser thr gly gly leu tyr glu thr val asn glu
1921
1951
GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC
val tyr lys leu val ile pro ile leu glu ala his arg glu phe arg lys leu thr leu
1981
2011
ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG
thr his ser lys leu gln arg ala phe asp ser ile val asn lys asp his lys arg met
2041
2071
TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT GGG GAT TTG GAT GAA CAG
phe gly thr tyr phe arg val gly phe phe gly ser lys phe gly asp leu asp glu gln
2101
2131
GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC AAG TTT CCT GAG ATC TCA CAT AGA CTA GAG
glu phe val tyr lys glu pro ala ile thr lys leu pro glu ile ser his arg leu glu
2161
2191
GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT
ala phe tyr gly gln cys phe gly ala glu phe val glu val ile lys asp ser thr pro
ref 4.1
2221
2251
GTG GAT AAA ACC AAG TTG GAT CCT AAT AAG GCC TAC ATA CAG ATC ACT TTT GTG GAG CCC
val asp lys thr lys leu asp pro asn lys ala tyr ile gln ile thr phe val glu pro
2281
2311
TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC
tyr phe asp glu tyr glu met lys asp arg val thr tyr phe glu lys asn phe asn leu
2341
2371
2401
2431
GAA GAA TAT AGA AGG AAC ACA GTC TTG ATT ACT ATG CAC GCC TTC CGG TAC ATC AAG ACC
glu glu tyr arg arg asn thr val leu thr thr met his ala phe pro tyr ile lys thr
2461
2491

FIG. 4A (3 of 7)

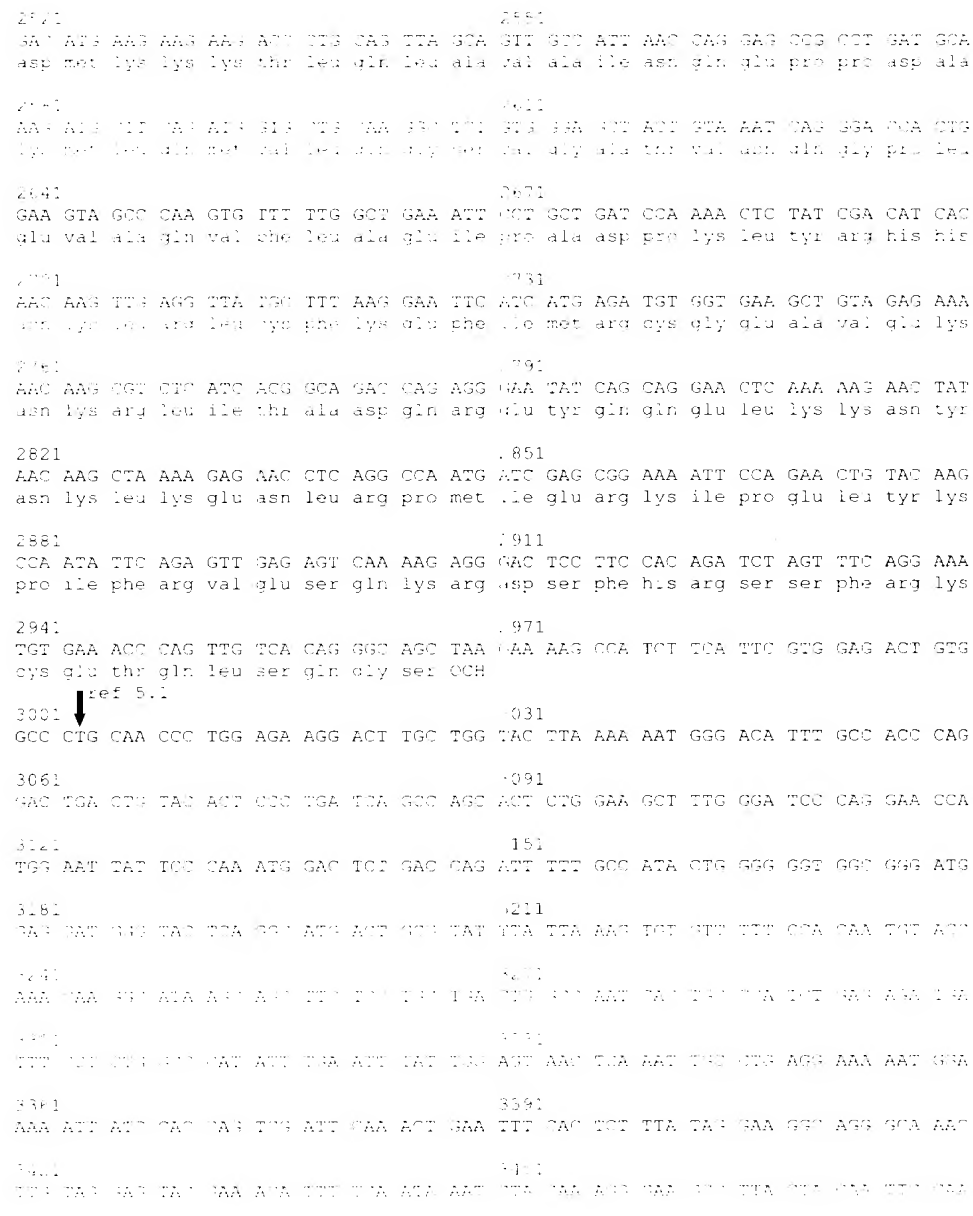
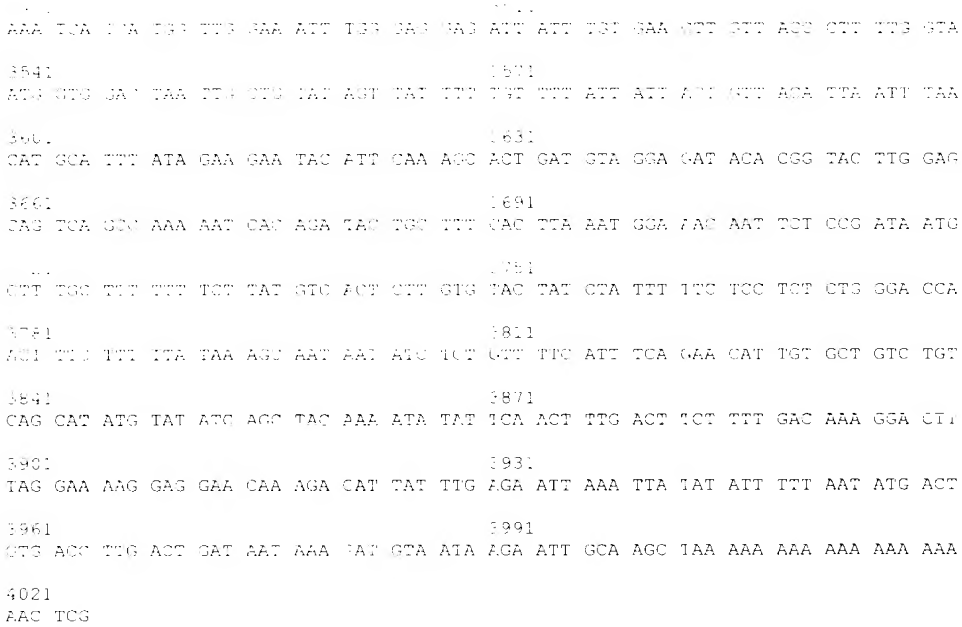


FIG. 4A (4 of 7)



Ref 1.1
Sequence of BAC19 using primer HC5S11, which spans nucleotides 3-22 of the cDNA.Exon sequence is underlined and represents nucleotides 32-57.

CTCTCTGTCTTCATATCTTCCAGGTTATAAAGNATTATTTACTAAAAGAANATTCANGC
TATTTCATTTAACTAGCTCAGTTTAATCATGTATTTCCTATAAAGGTTAGTCTTATTAAT
TTGACAAAACAATCAAACAATTCAAACCAGATCAAGTATGCTACCCTGAAGTTACACC
ACTAGTAAGAATTAATAATCTAAGTAATTGGTTTCTCCCCAGGCTCAAGGCTCCCTGA
TTAAGTTAAGTAAAGTCAACAATCCAATAAGCCCTATGAAATTTAGAAACTCATAGAA
AATTTTAAATTTTTTTTTTTCTCAGATTAAGCAATTGTTATATTATGCAAATAGAGGATT
NTAATAAAATAATTTGGAAGCTGTTTAGCAGGTTTTTGCAGCAGNCCTCTAAGAGCTT
AACTGGTCATGCATTGAATGCCGAGAGCAAAGAGGAATGGAGAGGGGNTGTAAGNGG
TTCCAATNTTACTGGAACCCACCACTATCTTTNGAAGTCTTGATACTTAACTGNGTGTA
TNTTNTTTATGTTNTANTAANTAGAATTTATATTGATTCGTGTTCTTTGNGTAAGNAG
TGCCTATGAAA

FIG. 4A (5 of 7)

Ref 2.1
Sequence of BAC19 using primer H05A610b, which spans nucleotides 56[illegible]-58[illegible] of Exon sequence is underlined and represents nucleotides 510-553.

Ref 3.1
Sequence of BAC19 using primer 0533, which spans nucleotides 10[illegible]-1115 of the cDNA. Exon sequence is underlined and represents nucleotides 1113-1120.

Ref 4.1
Sequence of BAC19 using primer C887, which spans nucleotides 11[illegible]-2203 of the cDNA. . Exon sequence is underlined and represents nucleotides 2220-2231.

FIG. 4A (6 of 7)

CCANNAGATTNTTGNAACGNNGGTAGGCTTCCTTTGTAGATTTATTGAAAATGTTTCGT
ACTTCTACAAGTTTGCCCTGCCTTCCTATAAAGAGTGAAANTCANTTTGAATCGACTGG
TGGATAATTNTTCCATTTTTTCCTCAGGCAATTTNGAGTTACTCCAATAAATTCAAATAT
GGGCCAGAGGAAATCATCTTTCAGATGGGCAGTGATTGGCCAGTCAGCAGGAGAAGC
TGCTTATGCCTTGTTTGGTACATTGTGGAAAAACACACTTTAATAAATACGCANTCATG
CCTGAGTACCCATCCTCCATCCCGCCACCCCCCAGTATGGCAAAAATCTGGTCAGAGT
CCATTTGGGAATAATTCCATGGTTCCTGGGATCCCAAAGCTTCCAGAAGTGCTGGCTG
ATCAANGGAGTGTACAGTCAGTCCTGCGTGGCAAAAATGTCCCATTTTTTAAGTACCA
AGCAAAGGTTCCTTCTTNCAAGGGTTNCTAGGGCC

FIG. 4A (7 of 7)

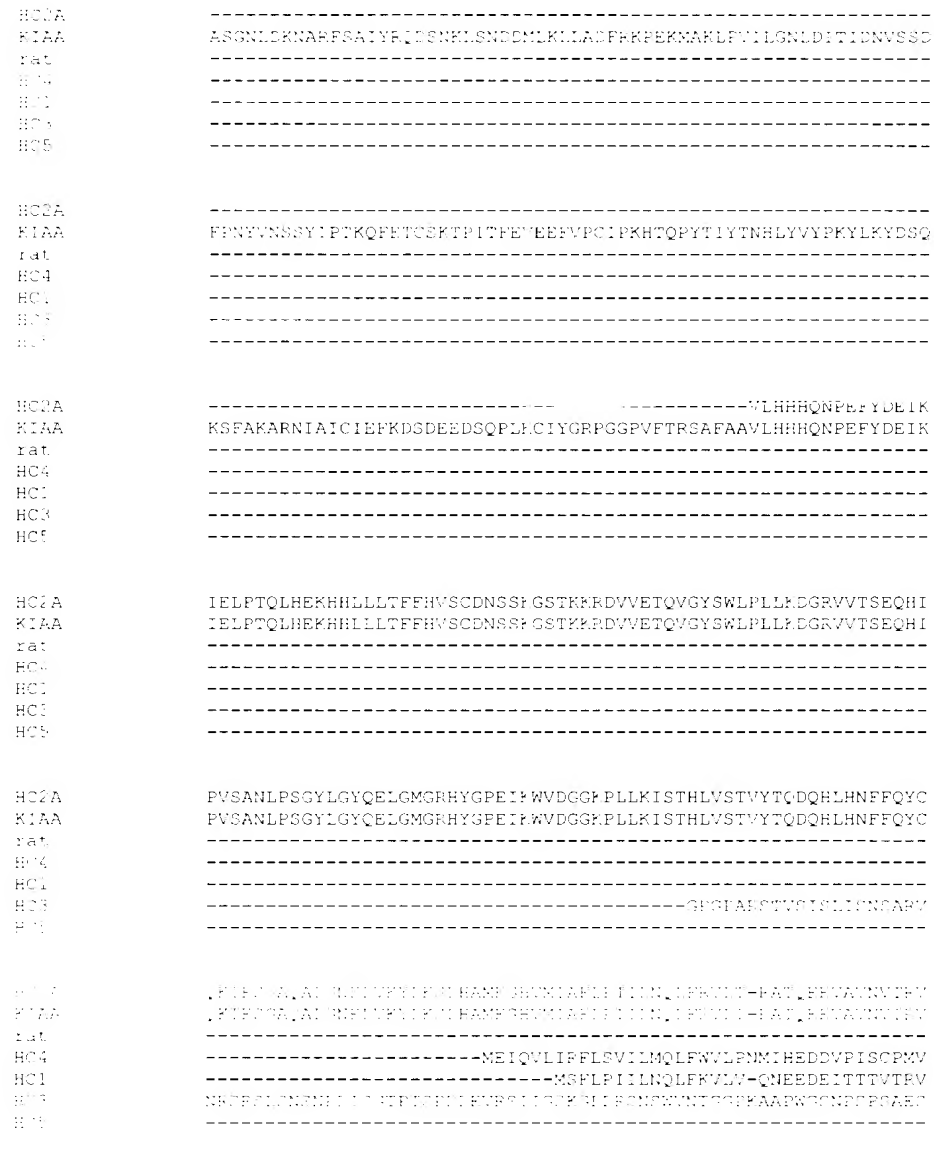


FIG. 4B (1 of 5)

FIG. 4B (2 of 5)

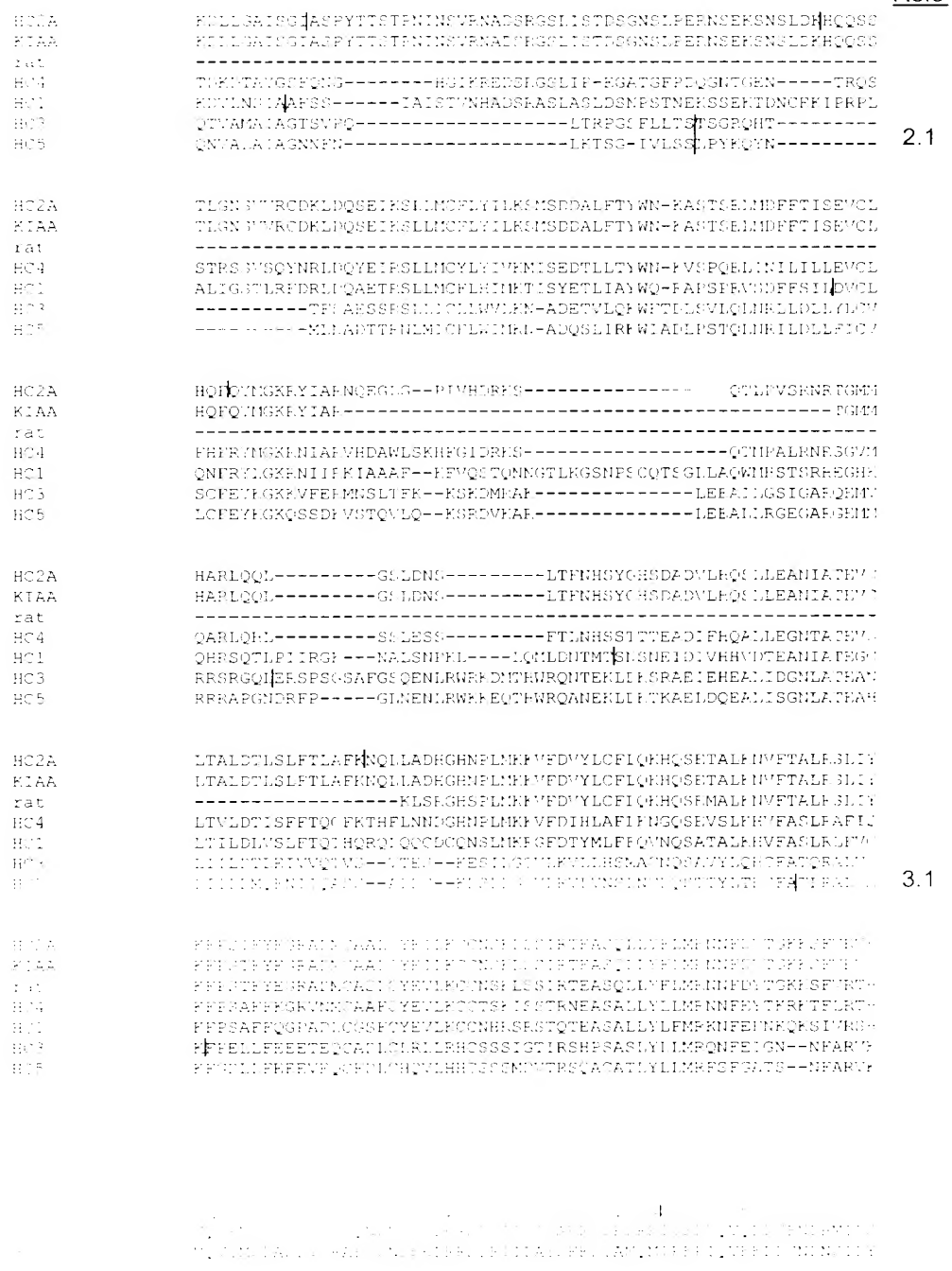


FIG. 4B (3 of 5)

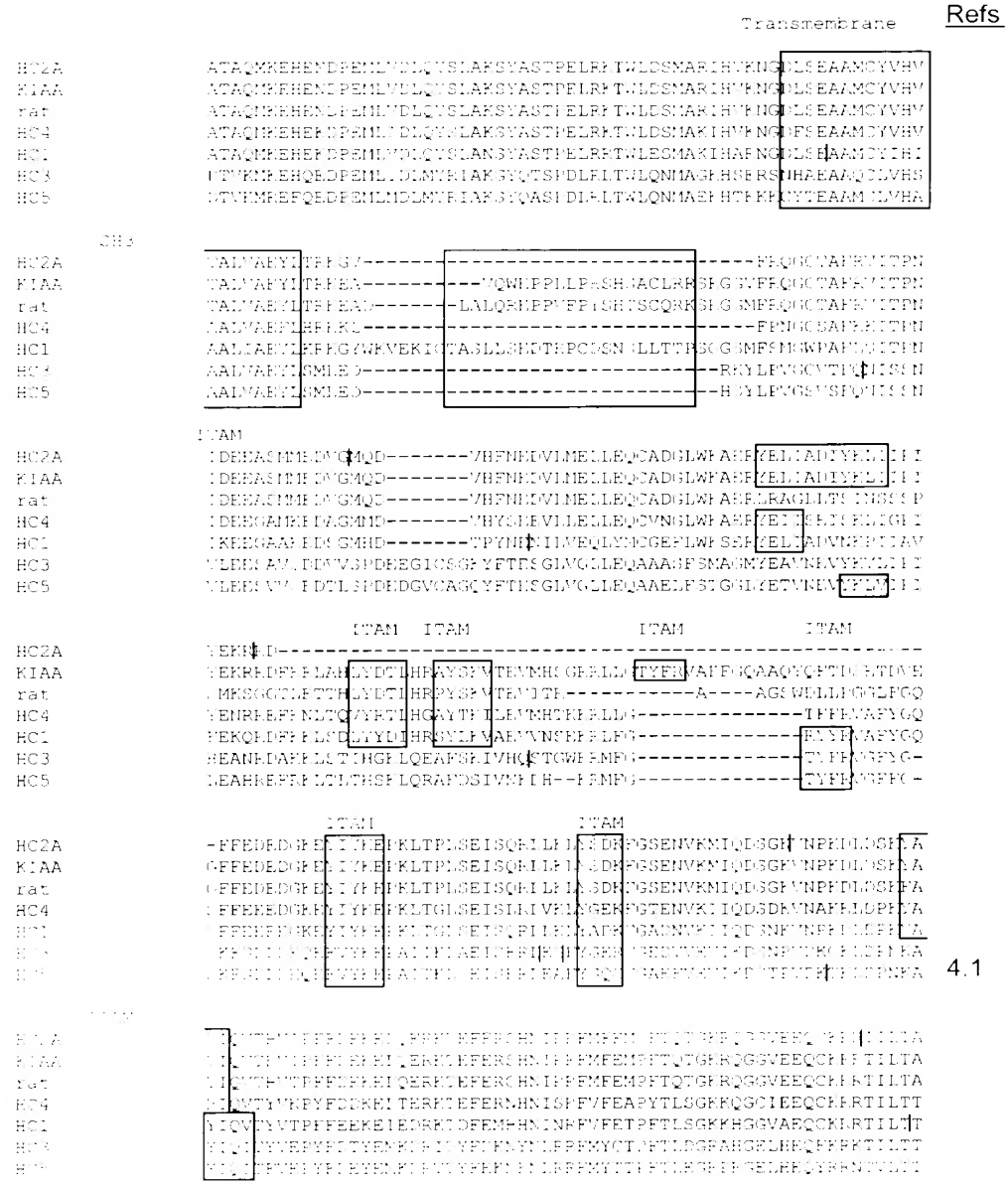

Transmembrane
Refs
HC2A
KIAA
rat
HC4
HC1
HC3
HC5
ITAM
ITAM
ITAM
ITAM
ITAM
ITAM
4.1

FIG. 4B (4 of 5)

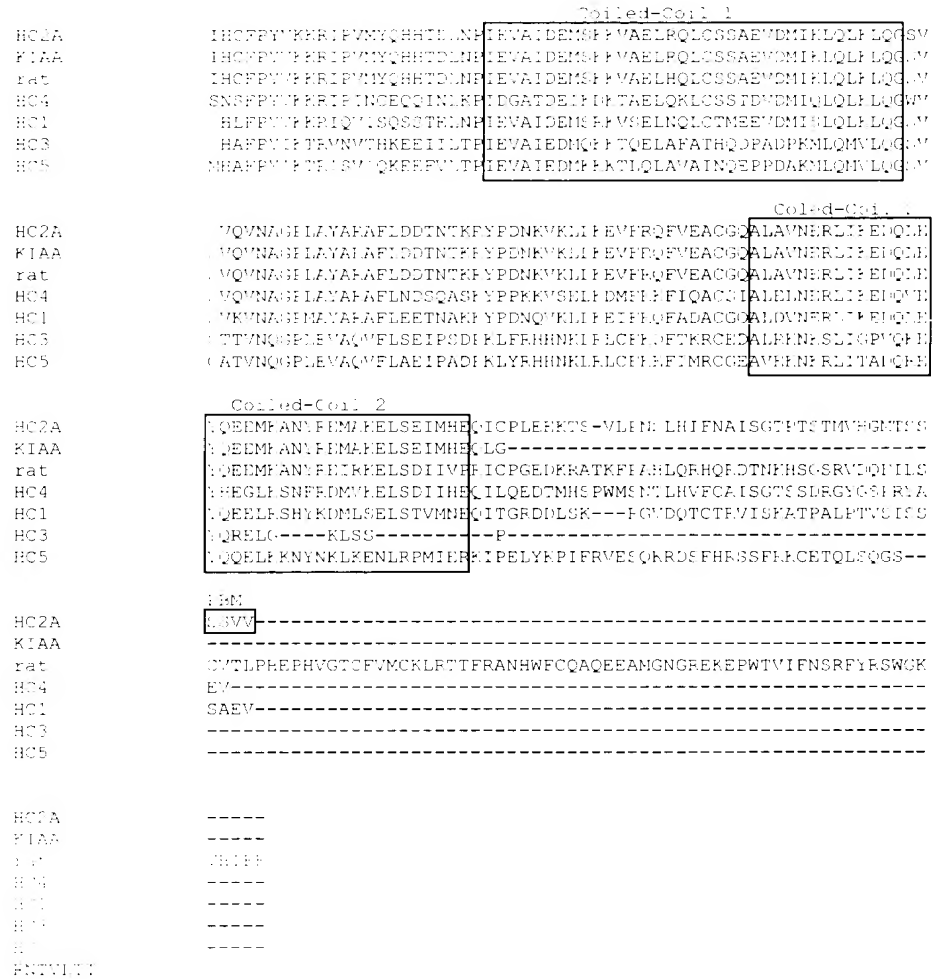


FIG. 4B (5 of 5)

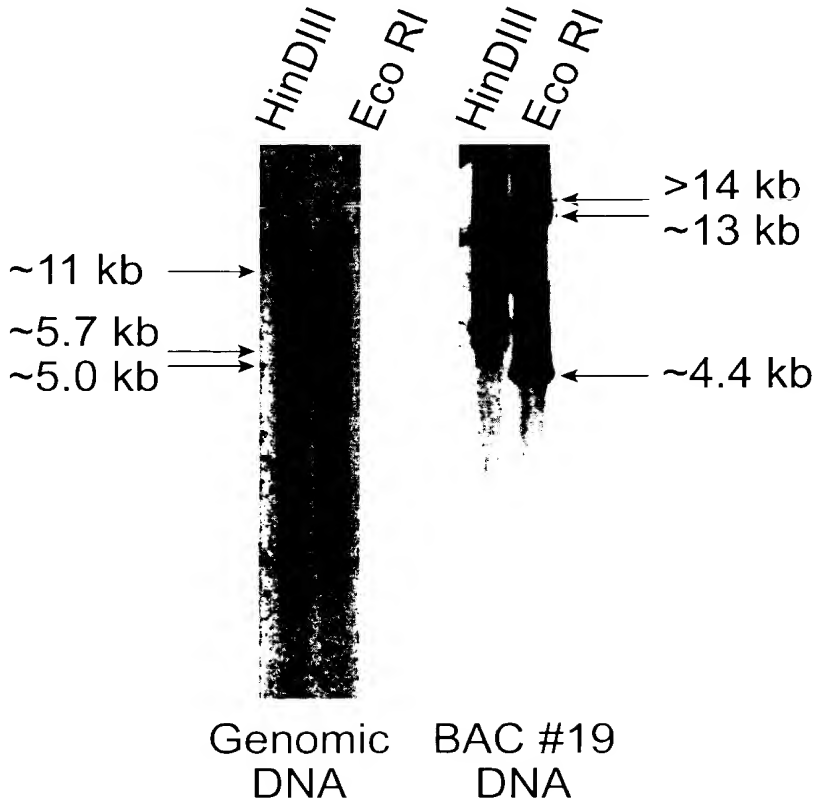

HinDIII
Eco RI
HinDIII
Eco RI
>14 kb
~13 kb
~11 kb
~5.7 kb
~5.0 kb
~4.4 kb
Genomic DNA
BAC #19 DNA

FIG. 5

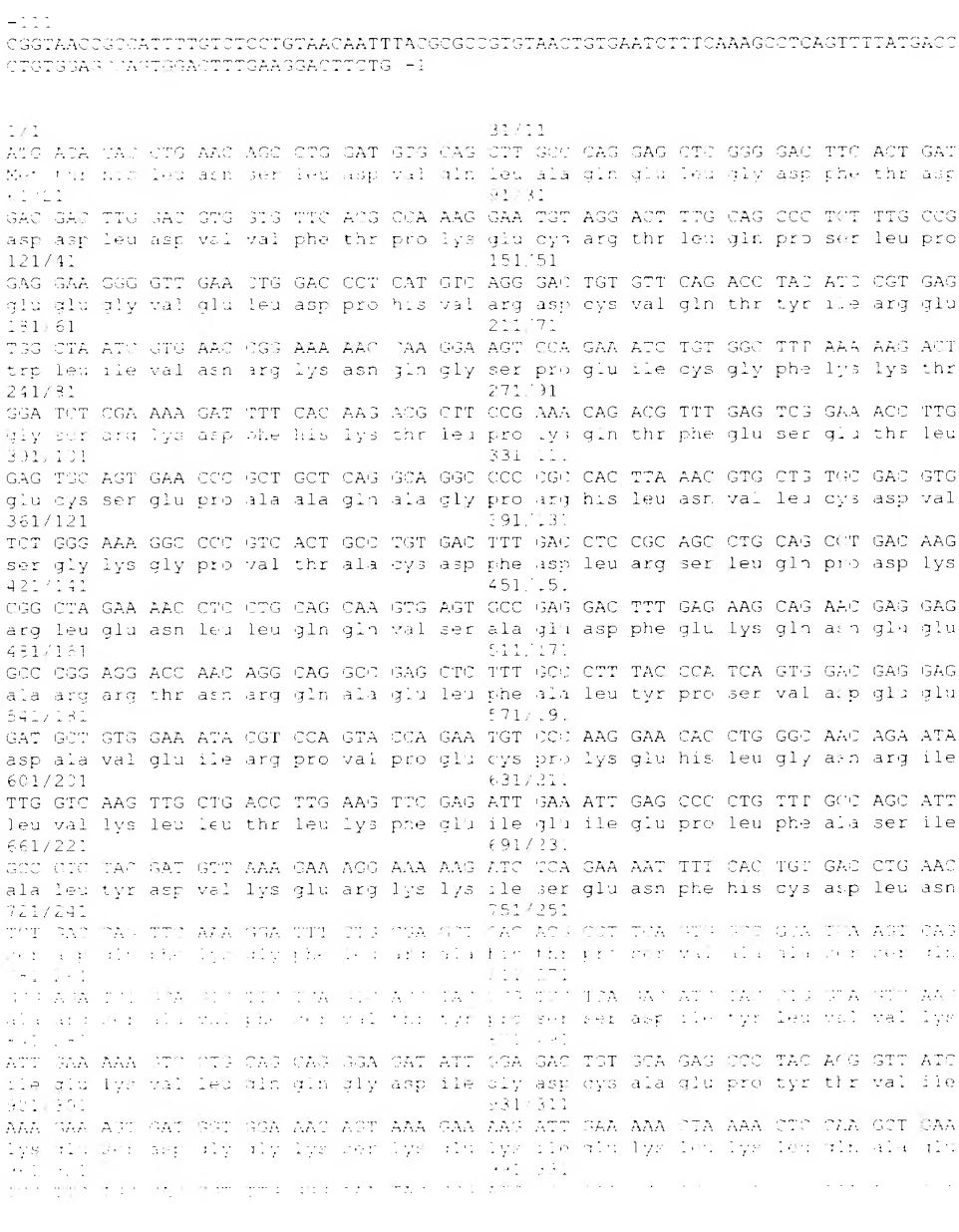


FIG. 6A (1 of 6)

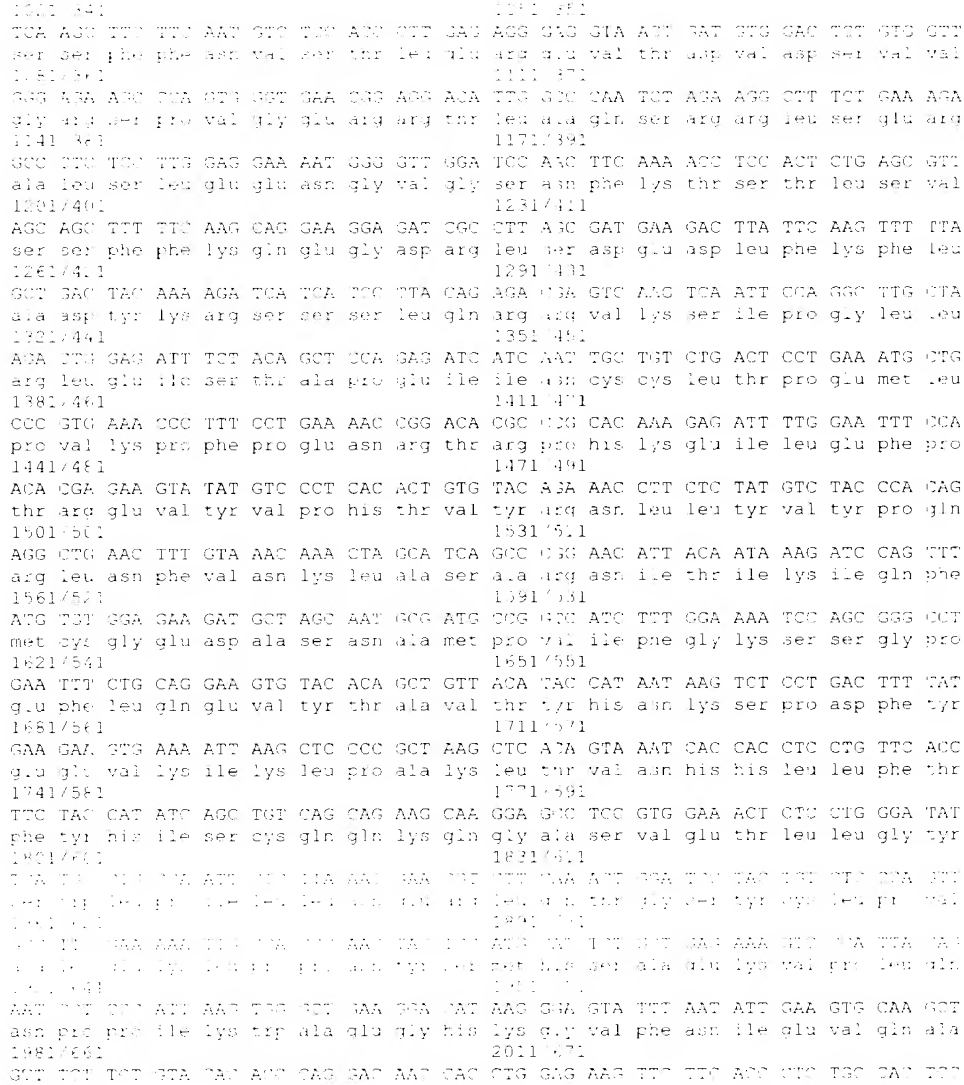


FIG. 6A (2 of 6)

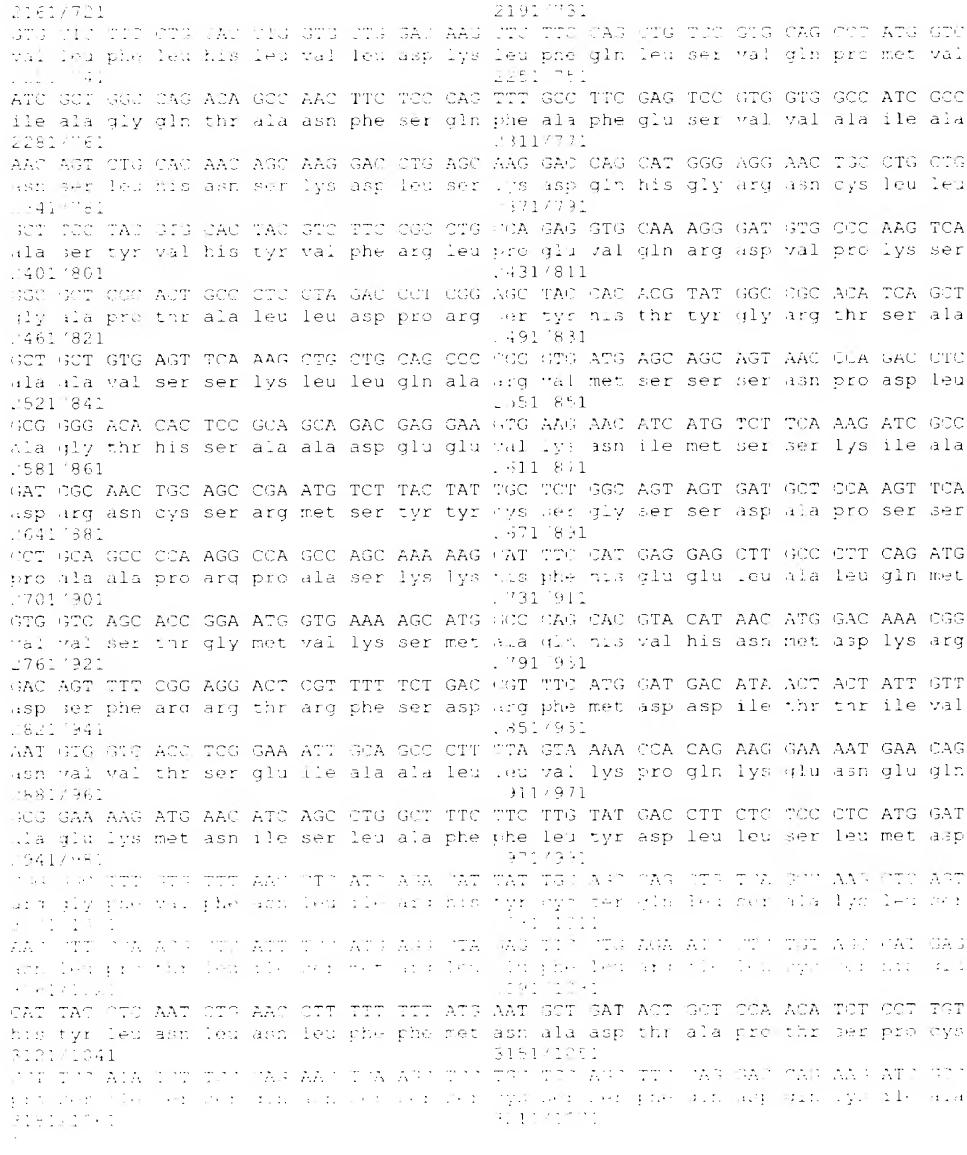


FIG. 6A (3 of 6)

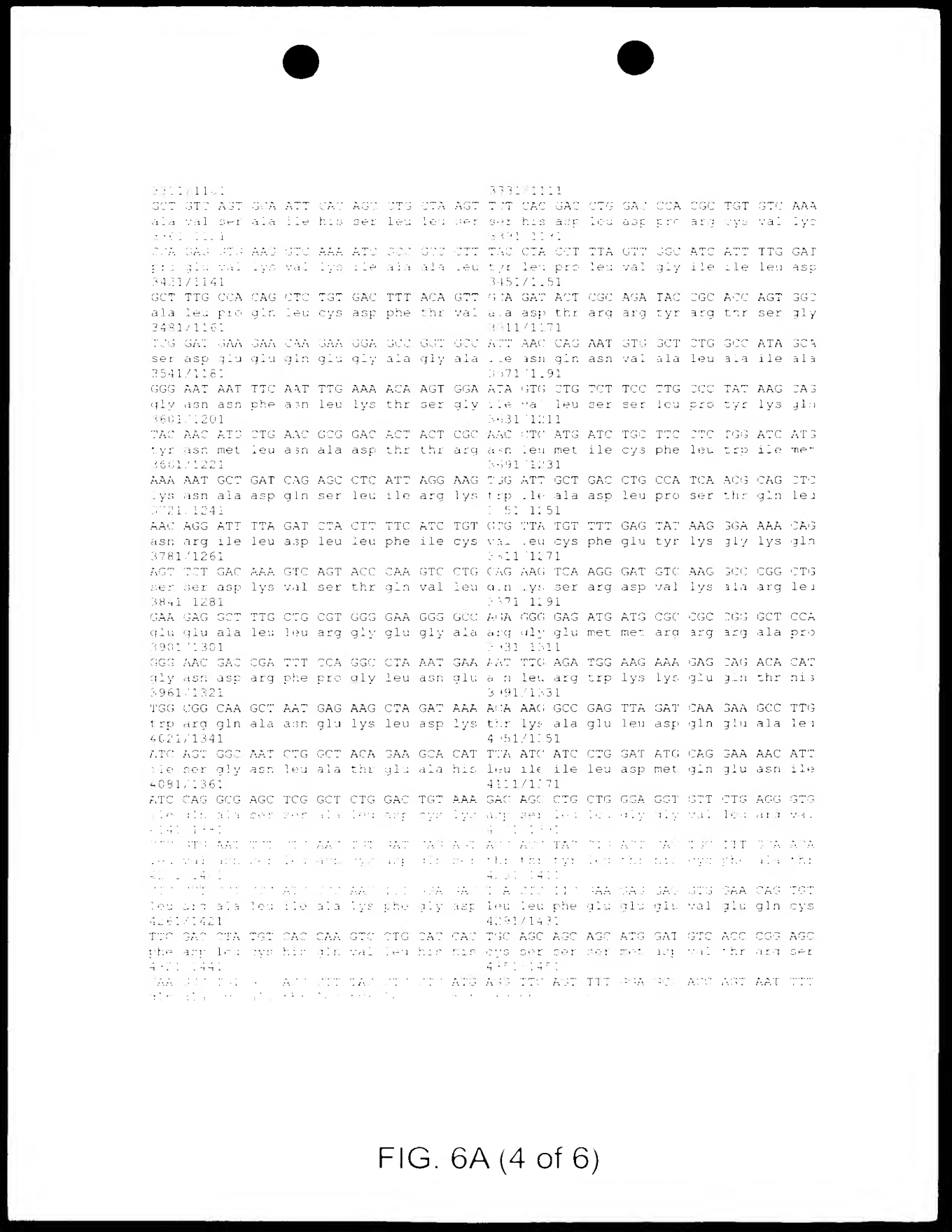


FIG. 6A (4 of 6)

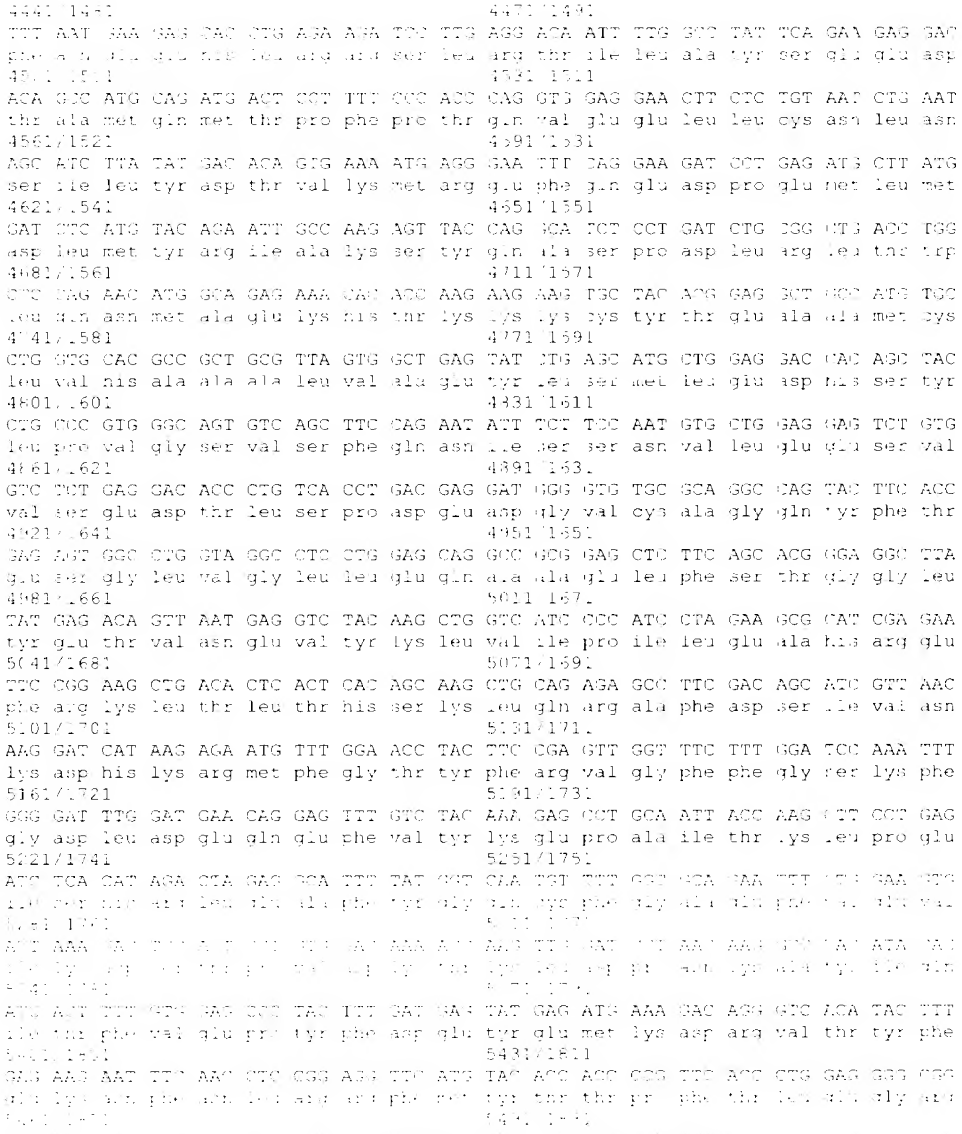


FIG. 6A (5 of 6)

```
5561/1861                                   5611/1871
ATT GAA GTT GCT ATT GAA GAC ATG AAG AAG     AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC
Ile Glu Val Ala Ile Glu Asp Met Lys Lys     Lys Thr Leu Gln Leu Ala Val Ala Ile Asn
5641/1881                                   5671/1891
CAG GAG CCG CCT GAT GCA AAG ATG CTT CAG     ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT
Gln Glu Pro Pro Asp Ala Lys Met Leu Gln     Met Val Leu Gln Gly Ser Val Gly Ala Thr
5701/1901                                   5731/1911
GTA AAT CAG GGA CCA CTG GAA GTA GCC CAA     GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA
Val Asn Gln Gly Pro Leu Glu Val Ala Gln     Val Phe Leu Ala Glu Ile Pro Ala Asp Pro
5761/1921                                   5791/1931
AAA CTC TAT CGA CAT CAC AAC AAG TTG AGG     TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT
Lys Leu Tyr Arg His His Asn Lys Leu Arg     Leu Cys Phe Lys Glu Phe Ile Met Arg Cys
5821/1941                                   5851/1951
GGT GAA GCT GTA GAG AAA AAC AAG CGT CTG     ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG
Gly Glu Ala Val Glu Lys Asn Lys Arg Leu     Ile Thr Ala Asp Gln Arg Glu Tyr Gln Gln
5881/1961                                   5911/1971
GAA CTC AAA AAG AAC TAT AAC AAG CTA AAA     GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA
Glu Leu Lys Lys Asn Tyr Asn Lys Leu Lys     Glu Asn Leu Arg Pro Met Ile Glu Arg Lys
5941/1981                                   5971/1991
ATT CCA GAA CTG TAC AAG CCA ATA TTC AGA     GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC
Ile Pro Glu Leu Tyr Lys Pro Ile Phe Arg     Val Glu Ser Gln Lys Arg Asp Ser Phe His
6001/2001                                   6031/2011
AGA TCT AGT TTC AGG AAA TGT GAA ACC CAG     TTG TCA CAG GGC AGC TAA
Arg Ser Ser Phe Arg Lys Cys Glu Thr Gln     Leu Ser Gln Gly Ser OCH
```

```
GAAAAGCCATCTTCATTCGTGGAGACTGTGGCCCTGCAACCCTGGAGAAGGACTTGCTGGTACTTAAAAAATGGGACATT
TGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTCTGGAAGCTTTGGGATCCCAGGAACCATGGAATTATT
CCCAAATGGACTCTGACCAGATTTTTGCCATACTGGGGGGTGGCGGGATGGAGGATGGGTACTCAGGCATGACTGCGTAT
TTATTAAAGTGTGTTTTTCCACAATGTACCAAACAAGGCATAAGCAGCTTCTCCTGCTGACTGGCCAATCACTGCCCATC
TGAGAGATGATTTCCTCTGGCCCATATTTGAATTTATTGGAGTAACTCAAATTGCCTGAGGAAAAATGGAAAAATTATCC
ACCAGTCGATTCAAACTGAATTTCACTCTTTATAGGAAGGCAGGGCAAACTTGTAGGAGTACGAAACATTTTCAATAAAT
CTACAAAGGGAAGCCTTACTACAATTCCAAAAATCATCATGGTTGGAAATTTGGGAGGAGATTATTTGTGAACTTGTTAC
CCTTTTGGTAATGGTGGACTAATTGCTGTATAGTTATTTTTGTTTTATTATTACTGTTACATTAATTTAACATGCATTTA
TAGAAGAATACATTCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGCAGTCAGCCAAAAATCACAGATACTGCTTT
CACTTAAATGGAAACAATTCTCCGATAATGCTTTGCTTTTTTTCTTATGTCACTCTTGTGTACTATCTATTTTTCTCCTC
TCTGGGACCAAGTTTCTTTTTATAAAGCAATAATATCTCTGTTTTCATTTCAGAACATTGTGCTGTCTGTCAGCATATGT
ATATCAGCTACAAAATATATTCAACTTTGACTTCTTTTGACAAAGGACTTTAGGAAAAGGAGGAACAAAGACATTATTTG
AGAATTAAATTATATATTTTTAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAATTGCAAGCTAAAAAAA
AAAAAAAAAAAACTCG
```

FIG. 6A (6 of 6)

A. Allelic variant not single nucleotide changes (polymorphism) between CLASP-5 cDNA isoforms

Isoform	Nucleotide(s)	Consequence
1	1787	C to T change; mis-sense mutation changing codon from alanine to valine
2	1749	A to G change; silent mutation
3	2277	G to C change; silent mutation
4	2853	C to T change; silent mutation
5	3427	A to G change; mis-sense mutation changing codon from lysine to glutamic acid
6	3777	C to T change; silent mutation

B. Alternative splices

Isoform	Difference	Nucleotide(s)	Consequence
1	exon deletion	1806-1944	premature, in-frame stop codon leading to the production of a truncated, most likely soluble protein
2	exon insertion	between 2857 and 2858	additional, in-frame 48 nucleotide exon that contains a stop codon at the second codon, which would lead to a truncated, most likely soluble protein

These differences may be found separately or together in various combinations in the different human CLASP-5 isoforms

FIG. 6B

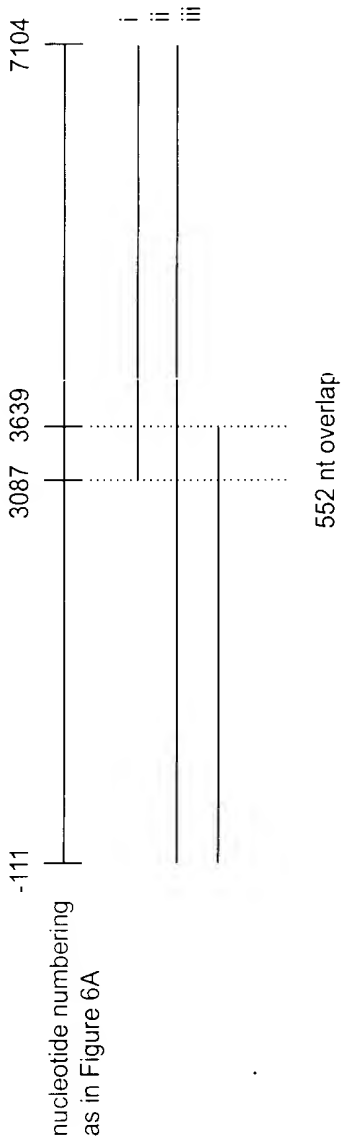

-111
3087
3639
7104
i
ii
iii
552 nt overlap
nucleotide numbering
as in Figure 6A

FIG. 6C

1st partial exon (nucleotides 3793 to 3952)
CCAGCTGTCAGCCAAGCTCAGTAACCTTCCAACGCTCATTTCCATGAGGCTAG
AGTTCCTGAGAATCCTCTCTGTAGCCATGAGCATTACCTCAATCTGAACCTTTTT
TTTATGAATGCTGATACTGCTGCAACATCTCCTTGTCCTTCCATATCTTCCCAG
GTAATAAAAGAATTATTTAACTAAAAGAATTATTCAAGCTAT

2nd exon (nucleotides 5809 to 5945)
GCTCATAAAATGGCTCCTTACGTTTCTGTAGAACTCAAGCTCCTGCTCCAGCT
TCCAGGACCAGAAGATCGCCAGCATGTTCGATCTGACTTCCGAGTACCGCCA
GTAGCACTTCCTCACCGGGCTCCTCTTCACAGAACTGGCTGCTGCCCTGGATG
CCGAAGGGAAGGGTATGTTTCTGGCATTAAAATGGAAGATGAAGC

3rd exin (nucleotides 13662 to 13831)
CATAACCTCTTGATTCCTGTGTTGTGCCAACAGAATCAGCAAAGTACAAAGG
AAAGCTGTCAGTGCAATTCACAGCCTGCTAAGTTCTCACGACCTGGACCCA
GCTGTGTCAAACCAGAGGTGAAGGTCAAAATGGCGCGCCTTTACCTACCTTTA
GTTGGCATCATTTTGGATGCTTTGCCACAGCTCTGTGACTTTACAGGTAATGG
CCCTTCTGTTCTCTTCCTTGGATTG

4th exin (nucleotides 16948 to 17097)
TGTTTTGACTTGACATCACAAACGATGTTTTCATTGCAGTTGCAGATACTCGCA
GATACCGCACCAGTGGCTCGGATGAAGAACAAGAAGGAGCCGGTGCCATTA
ACCAGAATGTGGCTCTGGCCATAGCAGGGAATAATTTCAATTTGAAAACAAG
TGGAATAGTGCTGTCTTCCTTGCTATGTTGGTGCACATGTGTCTGGTTGATTTT
TCAT

5th exon (nucleotides 18381 to 19463)
TGGCCTCCATCCCCCAATCTGCCTCCCTTCAGCCCTATAAGCAGTACAACATG
CTGAACGGGAGCACTACTCGCAACCTCATGATCTGCTTCCTCTGGATCATGAA
AAATGCTGATCAGAGCCTCATTAGGAAGTGGATTGCTGACCTGCCATCAACG
CAGCTCAACAGGATTTTACATCTACTTTTCATCTGTGTGTTATGTTTTGAGTAT
AAGGTAAGTCTGGAGTGGGACATTTTATACCAGC

6th exon (nucleotides 19829 to 19958)
CACCAAAGGACATGTCCTCCTACCTCTGTCTTGTCCAGGGAAAACAGAGTTCT
GACAAAGTCAGTACCCAAGTCCTGCAGAAGTCAAGGGATGTCAAGGCCCGG
CTGGAAGAGCCTTTGCTGCGTGGGGAAGGGGCCAGAGGGCAGATGATGCGC
CGCCGGGCTCCAGGTGTGTTGGACTGGCCTTCCTGCTCTCTGTCAAGC

FIG. 7A (1 of 4)

7th exon (nucleotides 20929 to 21015)
TCAAATTCCTATCATCATTTCTTAACTCCTAGGGAACGACCGATTTCCAGGC
CTAAATCAAAACTTGAGATGGAAGAAAGACCAGACACATTGGCGGCAAGCT
AATGAGAAGCTAGATAAGTGAGTCACTTGGCAACTTTCTGCTACTTTTACCT

8th exon (nucleotides 25745 to 25861)
GCTTTAATTTGACCTCTTGTTGTTTCCTAGAACAAAGGCCGAGTTAGATCAAG
AAGCCTTGATCAGTGGCAATCTGGCTACAGAAGCACATTTAATCATCCTGGA
TATGCAGGAAAACATTATCCAGGTGAGGAAAACAAACACCCAATCTGATTTG

9th exon (nucleotides 27242 to 27376)
GGATTCAATGATGCCTTTCTTGCATTCCCCCAGGCGAGCTCGGCTCTGGACTG
TAAAGACAGCCTGCTGGAGGTGTTCTGAGGGTGCTGGTGAATTCTCTGAAC
TGTGATCAGAGTACCACCTACCTGACTCACTGCTTTGCAACACTCCGTGCTCT
CATCGCCAAGGTAAACTTGGGATGCTTGTTTTCTTCCTCTTAATT

10th exon (nucleotides 28582 to 28734)
AGTGATGCCTAATGGCCCTTTATGTCTCTCCTAGTTTGGAGACTTACTCTTCG
AAGAGGAGGTGGAACAGTGTTTCGACCTATGTCACCAAGTCCTGCACCACTG
CAGCAGCAGCATGGATGTCACCCGGAGCCAAGCCTGTGCCACCCTTACCTC
CTCATGAGGTTCAGTTTTGGAGCCACCAGTGTAAGAGTTCAAACCAGCTGAG
TGACCTGGAATCAG

11th exon (nucleotides 31044 to 31204)
TTACTTCACTCTTTTTTTTTTTTTTCACTGATGCAGAATTTTGCAAGAGTAAAGA
TGCAAGTAACCATGTCCCTGGCATCTTTGGTGGGAAGAGCACCAGACTTTAA
TGAAGAGCACCTGAGAAGATCCTTGAGGACAATTTTGGCCTATTCAGAAGAG
GACACAGCCATGCAGATGACTCCTTTTCCCACCCAGGTACACCGAAGCACAT
ACCTTGTCTCATGCATGAGT

12th exon (nucleotides 32755 to 32853)
AGTTAAAATTACTTTAAGCTTACACTTTTTGCAGCTGGAGGAACCTTCTCTG
AATCTGAATAGCATCTTATATCACACAGTTAAAATGAGGGAATTTCAGGAAG
ATCCTGAGATGCTTATGGATCTCATGTACAGGTAAGCTTTCCTGACACACCCA
AGGGACACCATTT

13th exon (nucleotides 33663 to 33855)
TCCTCAAAACTATCTTCTCACTCAATCTGTCTTCAGAATTGCCAAGAGTTACCA

FIG. 7A (2 of 4)

14th exon (nucleotides 38125 to 38268)
CTGTTCTCCAGGCTTATACTGTGGTCTCTTTCAGAATATTTCTTCCAATGTGCT
GGAGGAGTCTGTGGTCTCTGAGGACACCCTGTCACCTGACGAGGATGGGGTGTG
CGCAGCCCAGTACTTCACCGAGAGTGGCCTGGTAGGCCTCCTGGAGCAGG
CCGCGGAGCTCTTCAGCACGGTCAGTGCCCAGAGGGCATCCCGGGGCCTGGC
C

15th exon (nucleotides 40166 to 40297)
AATTCTCTCTGATGCTCTTCTCCTCTTCCAAGGGAGGCTTATAGGAGACAGT
TAATGAGGTCTACAAGCTGGTCATCCCATCCTAGAAGCGCATCGAGAATTC
CGGAAGTTGACACTCACTCACAGCAAGCTGCAGAGAGCCTTCGACAGCATCG
TTAACAAGGTAGCCGGGGAGCTCTGGCTGGCAGGTCTTGTTAC

16th exon (nucleotides 40755 to 40869)
TAAGGAGAGCTTTTTATATTTTGTTCCTCAGGATCATAAGAGAATGTTTGGAA
CCTACTTCCGAGTTGGTTTCTTTGGATCCAAATTTGGGGATTTGGATGAACAG
GAGTTTGTCTACAAAGAGCCTGCAATTACCAAGCTTCCTGAGATCTCACATAG
ACTAGAGGTAAGAAAAGTGATTCCGTGCGCCTGACCTGGTACACTTTAC

17th exon (nucleotides 42307 to 42396)
AACCTTTATAAACTGTTGGTTCTTCTTACCTAGGCATTTTATGGTCAATGTTTT
GGTGCAGAATTTGTGGAAGTGATTAAAGACTCCACTCCTGTGGACAAAACCA
AGTTGGATCCTAACAAGGTATACAAAAATTTACAAAAACTAACCATCAAGC

18th exon (nucleotides 45250 to 45486)
TCTTCTCCCTCCTGTGCCTTTTCCCCCTTAGGCCTACATACAGATCACTTTTGTG
GAGCCCTACTTTGATGAGTATGAGATGAAAGACAGGGTCACATACTTTGAGAAGA
ACTTCAAACTCCCGGAGGCTCATGTACACCAGCCCGTTCACCCTGGAGGG
GCGGCCTCGGGGAGAGCTGCATGAGCAGTACAGAAGGAACACAGTCCTGAC
GACTATGTACGCCTTCCCCCACATCAAGACCAAGATCAGCCTCATCCAGAAG
GAGGAGCTAATCCACCCAAGTGATTGGCACTCATTGGATGAGT

19th exon (nucleotides 48664 to 48807)
ACAGTGACTTCCCTATGTTTATGTTCATGTTCAGTTTGTTTTGACACCGATTG
AAGTTGCCATTGAAGACATGAAGAAGAAGACCCTGCAGTTAGCAGTTGCCAT
TAACAGGAGCCGCCTGATGCAAAGATGCTTCAGATGGTGCTGCAAGGCTCTGT
GGGAGCTACTGTAAATCAGGTAAGCAAAACCAGAGGTGGCAGCTCCT

[illegible]

FIG. 7A (3 of 4)

21st exon (nucleotides 62398 to 62568)

TCATTTATTTCTCCCACACTGATATTTTCATCTCAGATGTGGTGAAGCTGTAG
AGAAAAACAAGCGTCTCATCACGGCAGACCAGAGGGAATATCAGCAGGAAC
TCAAAAAGAACTATAACAAGCTAAAAGAGAACCTCAGGCCAATGATCGAGC
GGAAAATTCCAGAACTGTACAAGCCAATATTCAGAGTTGAGAGTCAAAAGAG
GTAAGAACAGGGCAGAGGAGGGCCTCTTCCTGTGGGAT

22nd exon (nucleotides 63040 to 63294)

CCTCCCTCTCTTTTCTTAATTTCAGGGACTCCTTCCACAGATCTAGTTTCAGGA
AATGTGAAACCCAGTTGTCACAGGGCAGCTAAGAAAAGCCATCTTCATTCGT
GGAGACTGTGGCCCTGCAACCCTGGAGAAGGACTTGCCGGTACTTAAAAAAT
GGGACATTTGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTC
TGGAAGCTTTGGGATCCCAGAACCATGGAATTATTCCCAAATGGACTCTGA
CCAGATTTTTGCCATACTGGGGGGTGGCGGGATGGAGGATGGGTACTCAGGC
ATGACTGCGTATCTATTAAAGTGTGTTTTTCCACAATGTACCAAACAAGGCAT
AAGCAGCTTCTCCTGCTGACTGGCCAATCACTGCCCATCTGAGAGATGATTTC
CTCTGGCCCATATTTGAATTTATTGGAGTAACTCAAATTGCCTGAGGAAAAAT
GGAAAAATTATCCACCAGTCGATTCAAACTGAATTTCACTCTTTATAGGAAG
GCAGGGCAAACTTGTAGGAGTACGAAACATTTTCAATAAATCTACAAAGGGA
AGCCTTACTACAATTCCAAAAATCATCATGGTTGGAAATTTGGGAGGAGATT
ATTTGTGAACTTGTTACCCTTTTGGTAATGGTGGACTAATTGCTGTATAGTTAT
TTTTGTTTTATTATTACTGTTACATTAATTTAACATGCATTTATAGAAGAATAC
ATTCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGCAGTCAGCCAAAA
ATCACAGATACTGCTTTCACTTAAATGGAAACAATTCTCCGATAATGCTTTGC
TTTTTTTCTTATGTCACTCTTGTGTACTATCTATTTTTCTCCTCTCTGGGACCAA
GTTTCTTTTTATAAAGCAATAATATCTCTGTTTTCCATTTCAGAACATTGTGCTG
TCTGTCAGCATATGTATATCAGCTACAAAATATATTCAACTTTGACTTCTTTTG
ACAAAGGACTTTAGGAAAAGGAGGAACAAAGACATTATTTGAGAATTAAATT
ATATATTTTTAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAA
TTGCAAGCTAAAAAAAAAAAAAAAAAA

FIG. 7A (4 of 4)

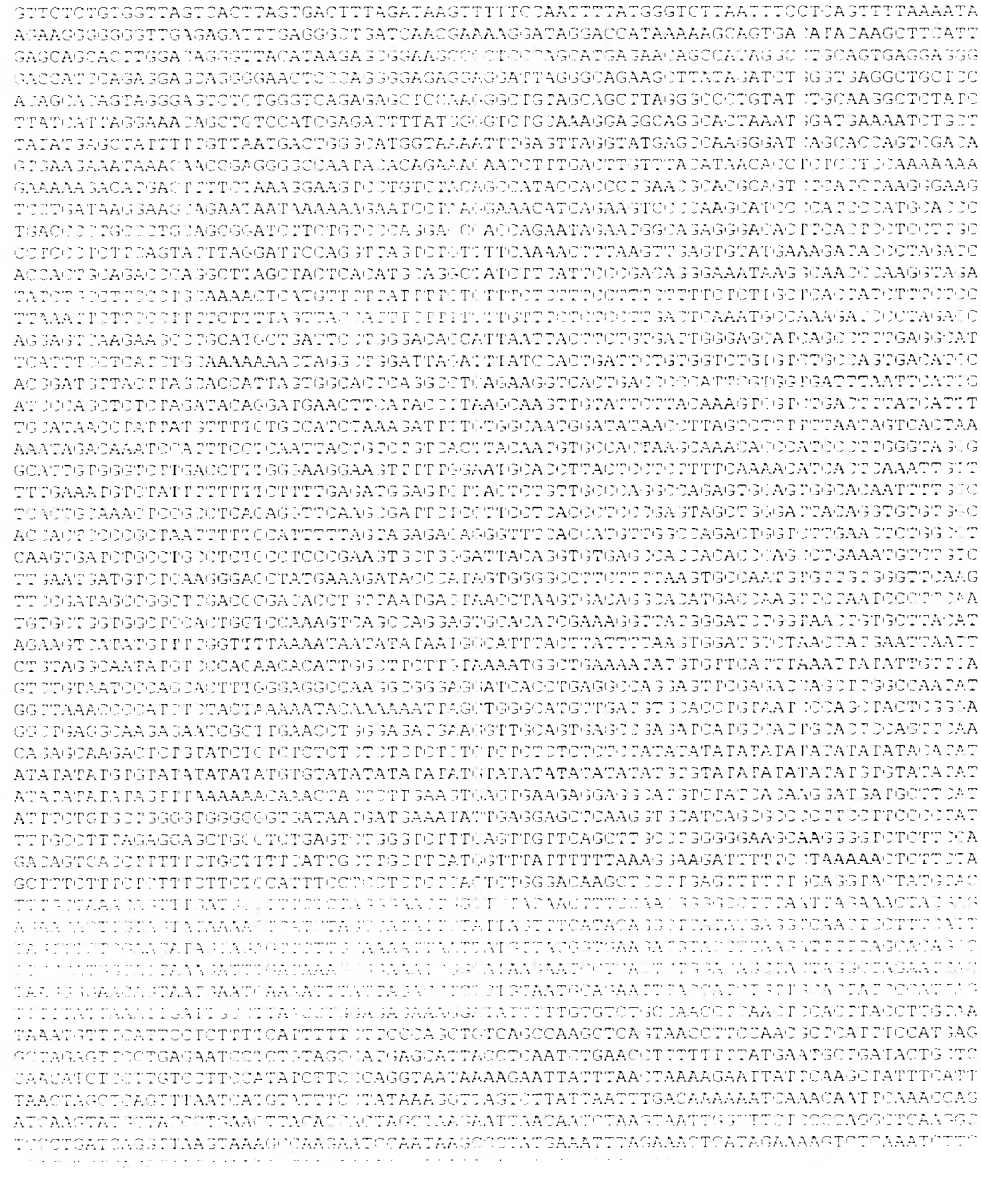


FIG. 7B (1 of 15)

FIG. 7B (2 of 15)

FIG. 7B (3 of 15)

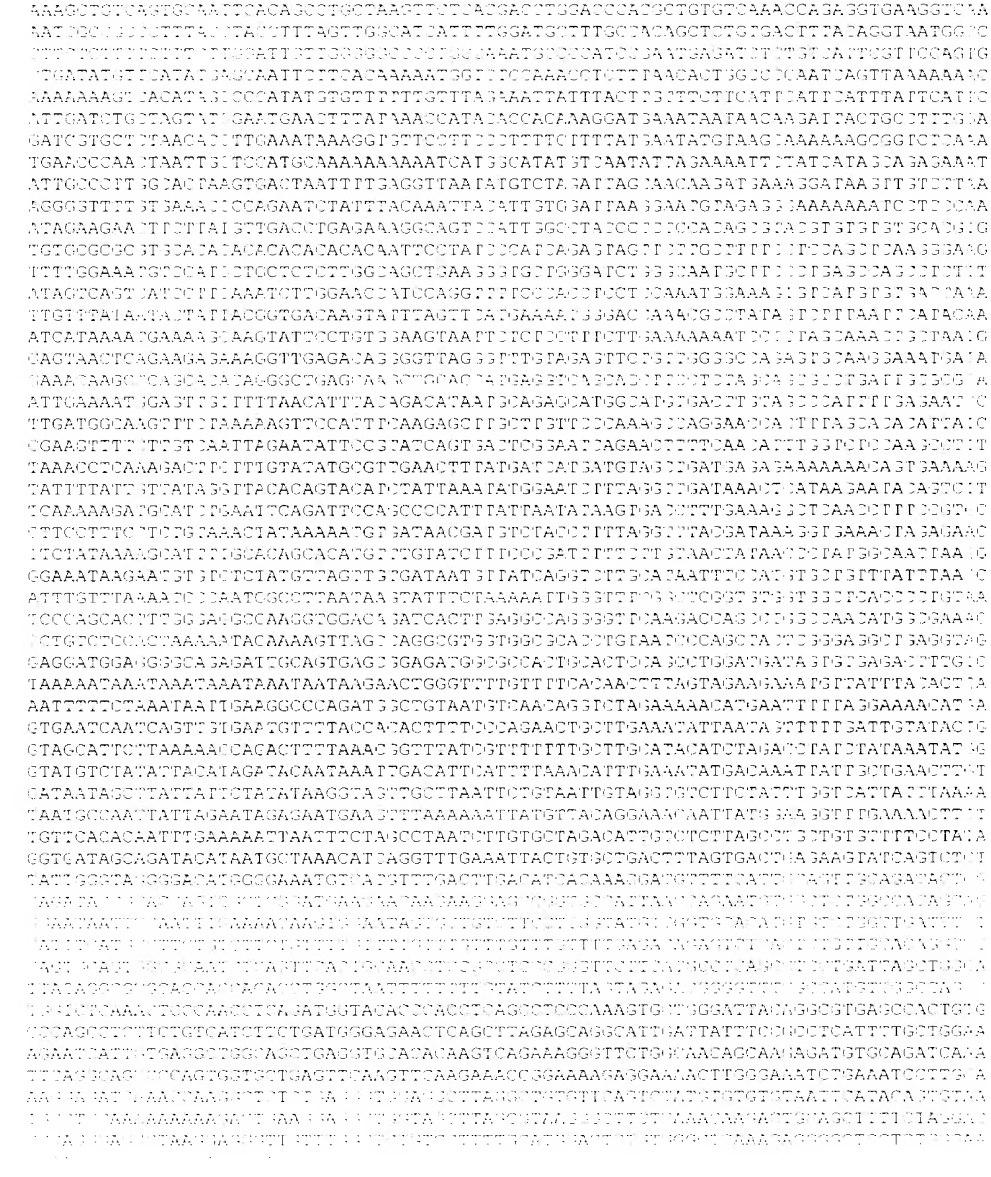


FIG. 7B (4 of 15)

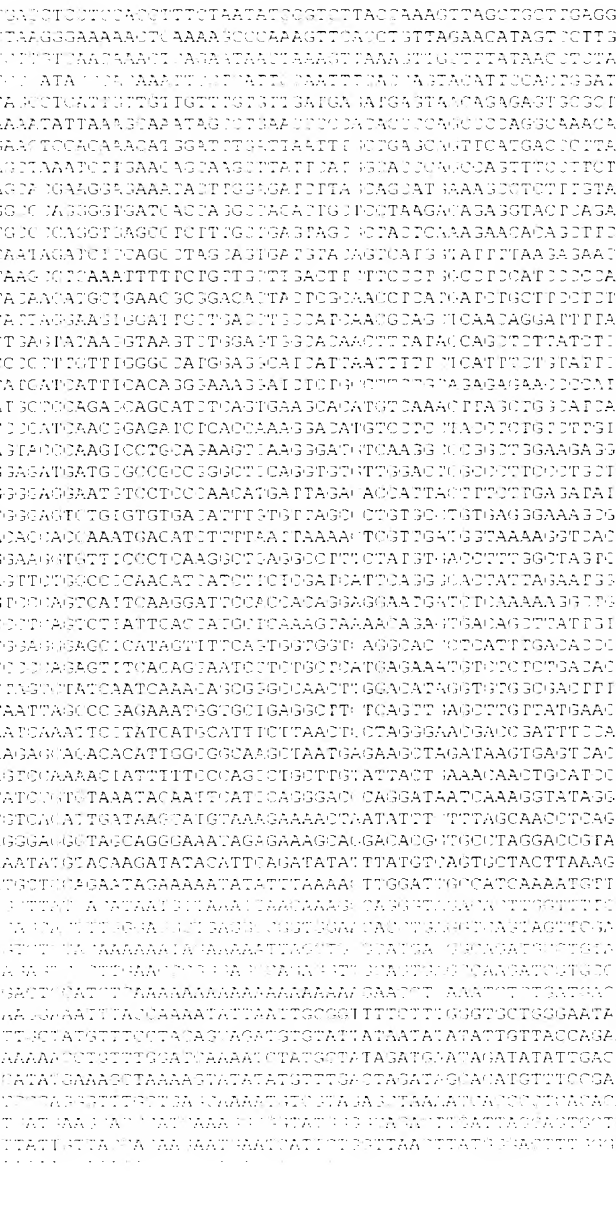


FIG. 7B (5 of 15)

FIG. 7B (6 of 15)

FIG. 7B (7 of 15)

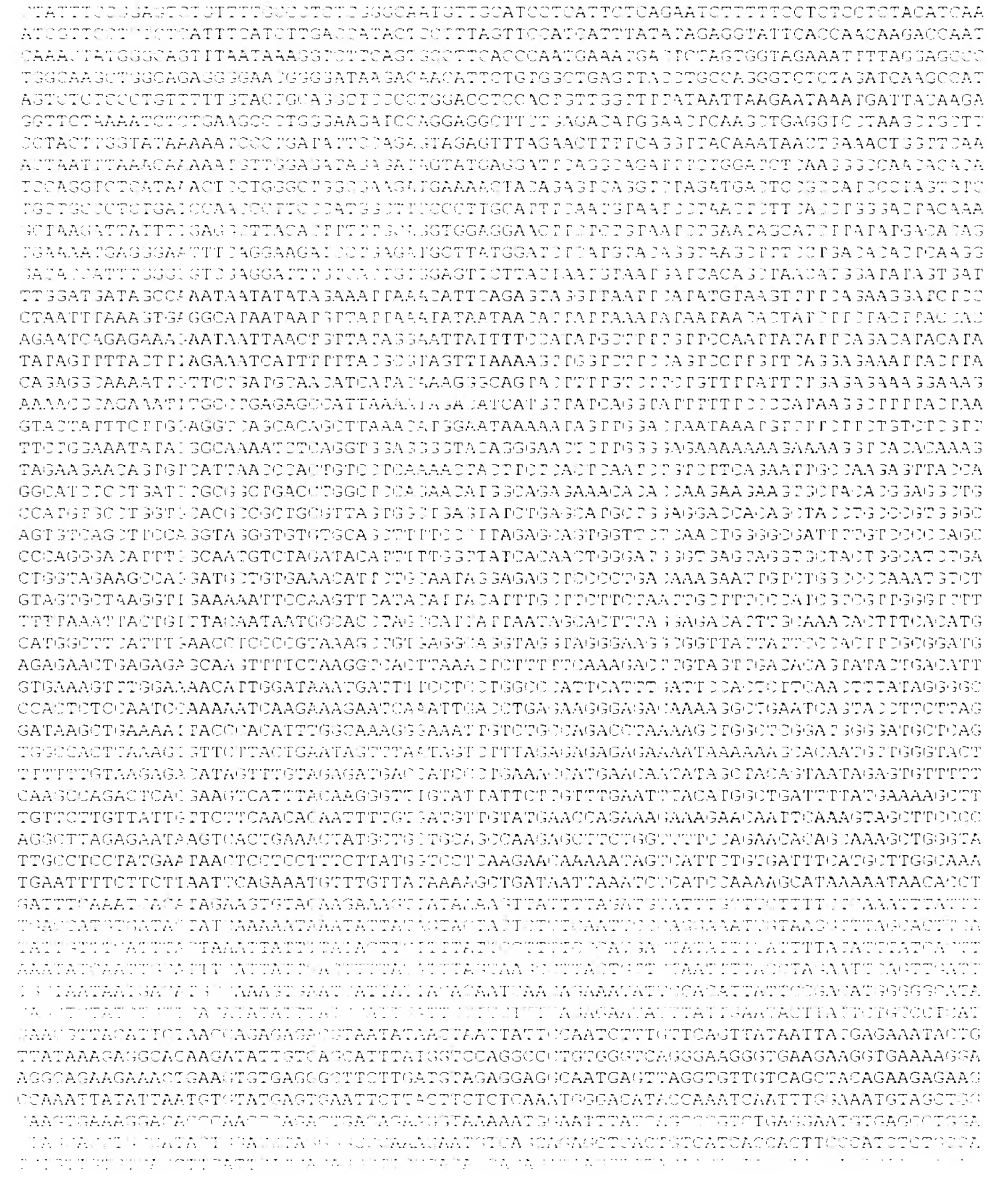


FIG. 7B (8 of 15)

FIG. 7B (9 of 15)

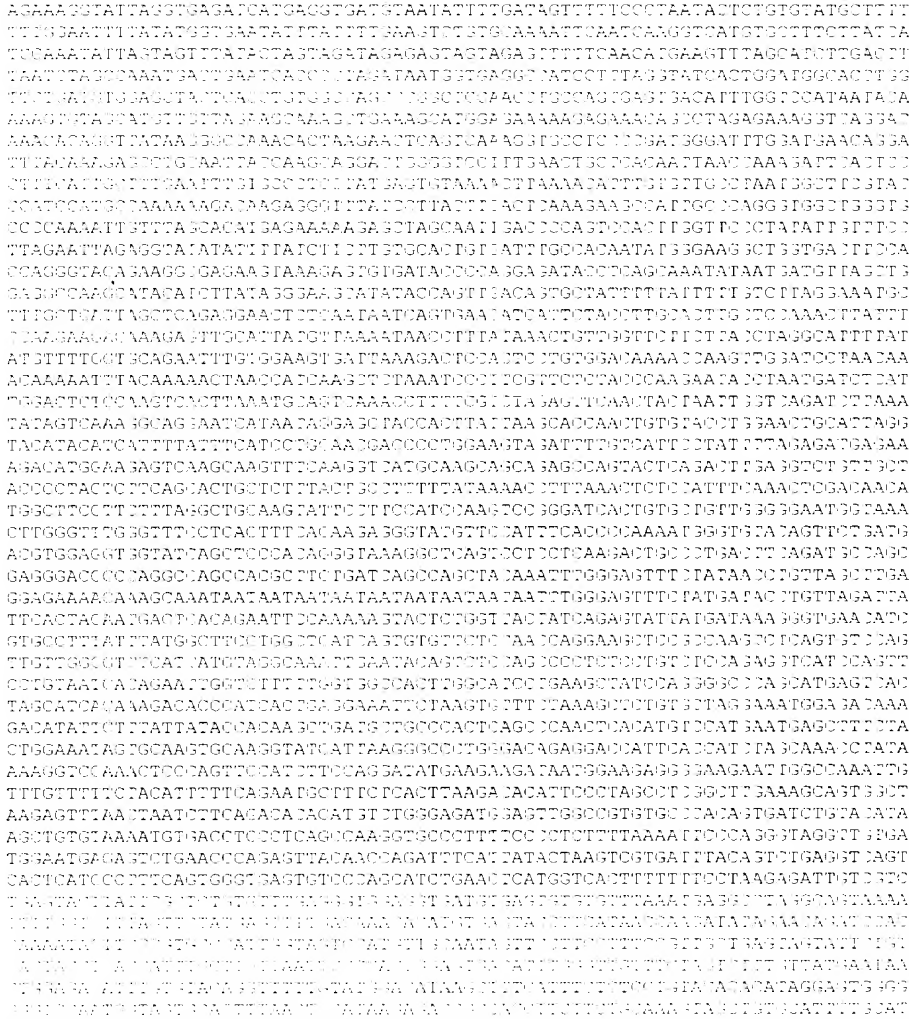


FIG. 7B (10 of 15)

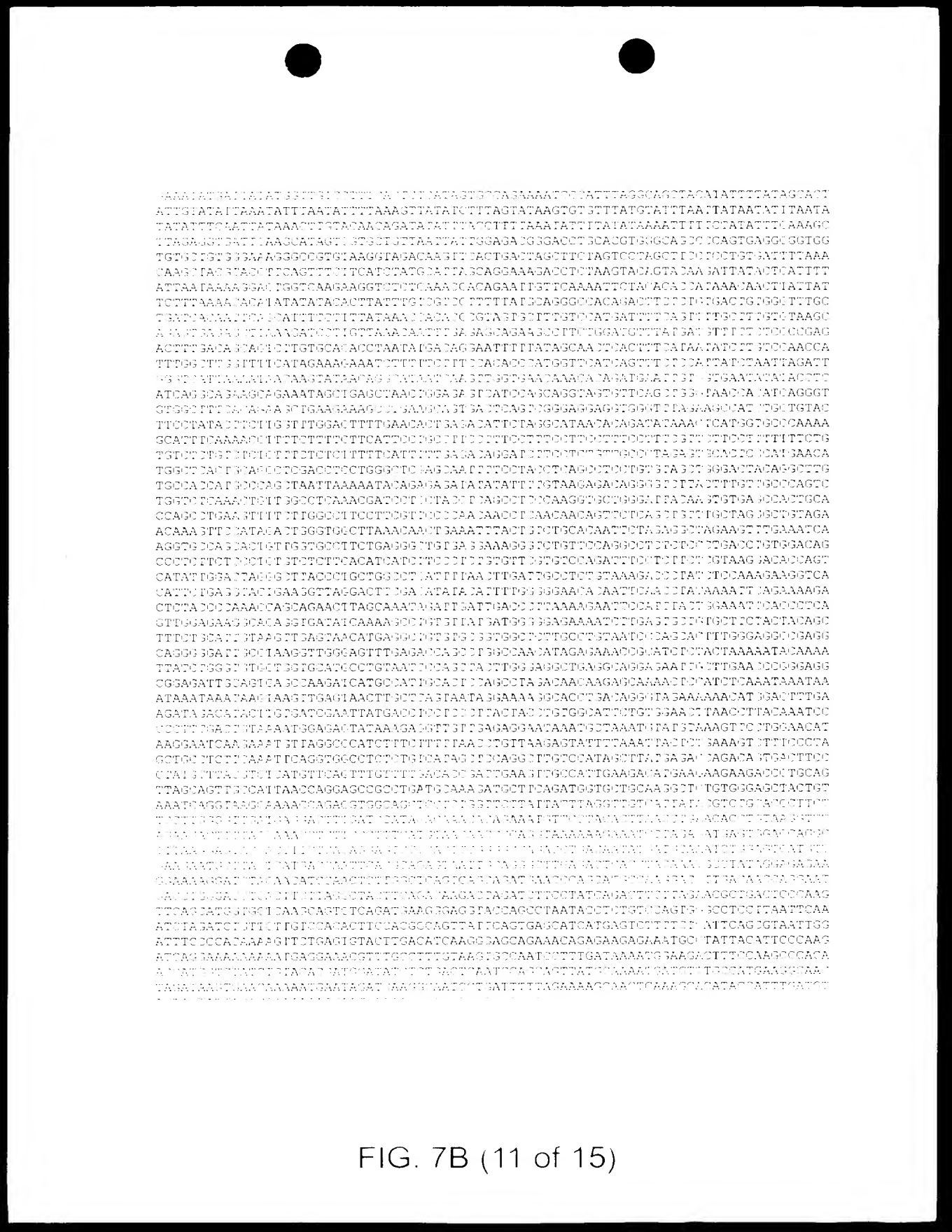


FIG. 7B (11 of 15)

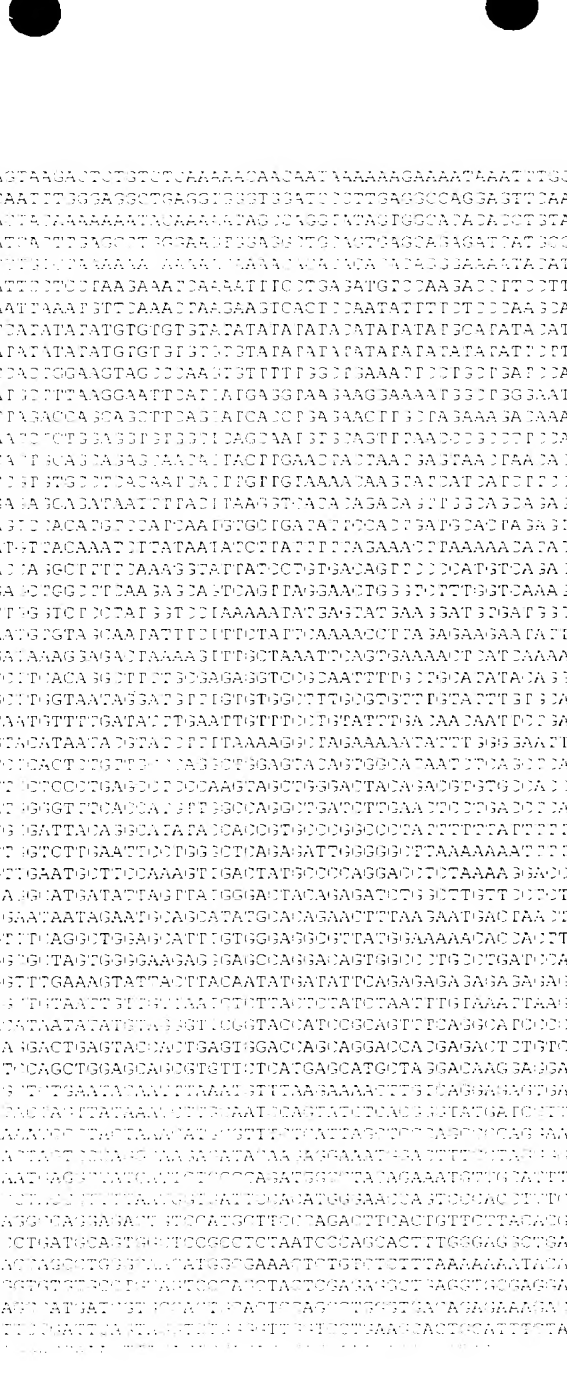


FIG. 7B (12 of 15)

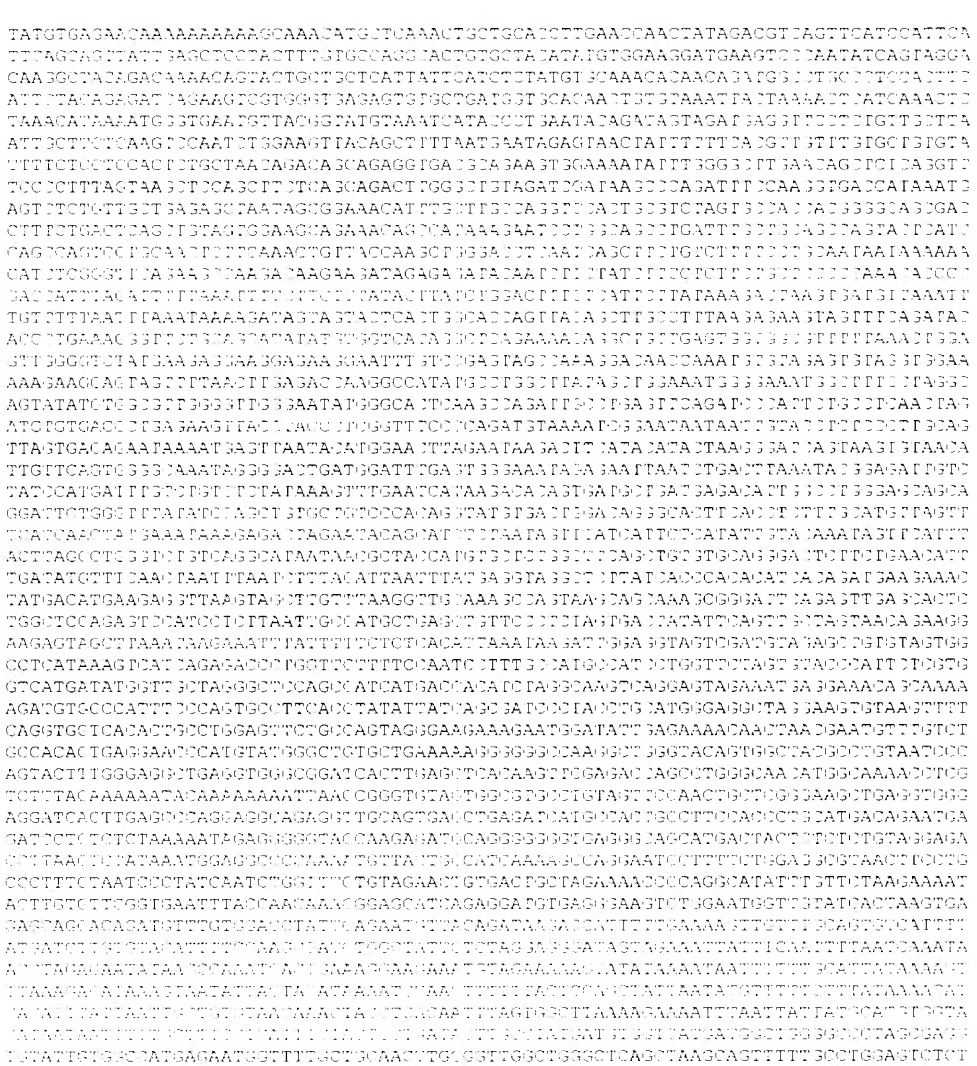


FIG. 7B (13 of 15)

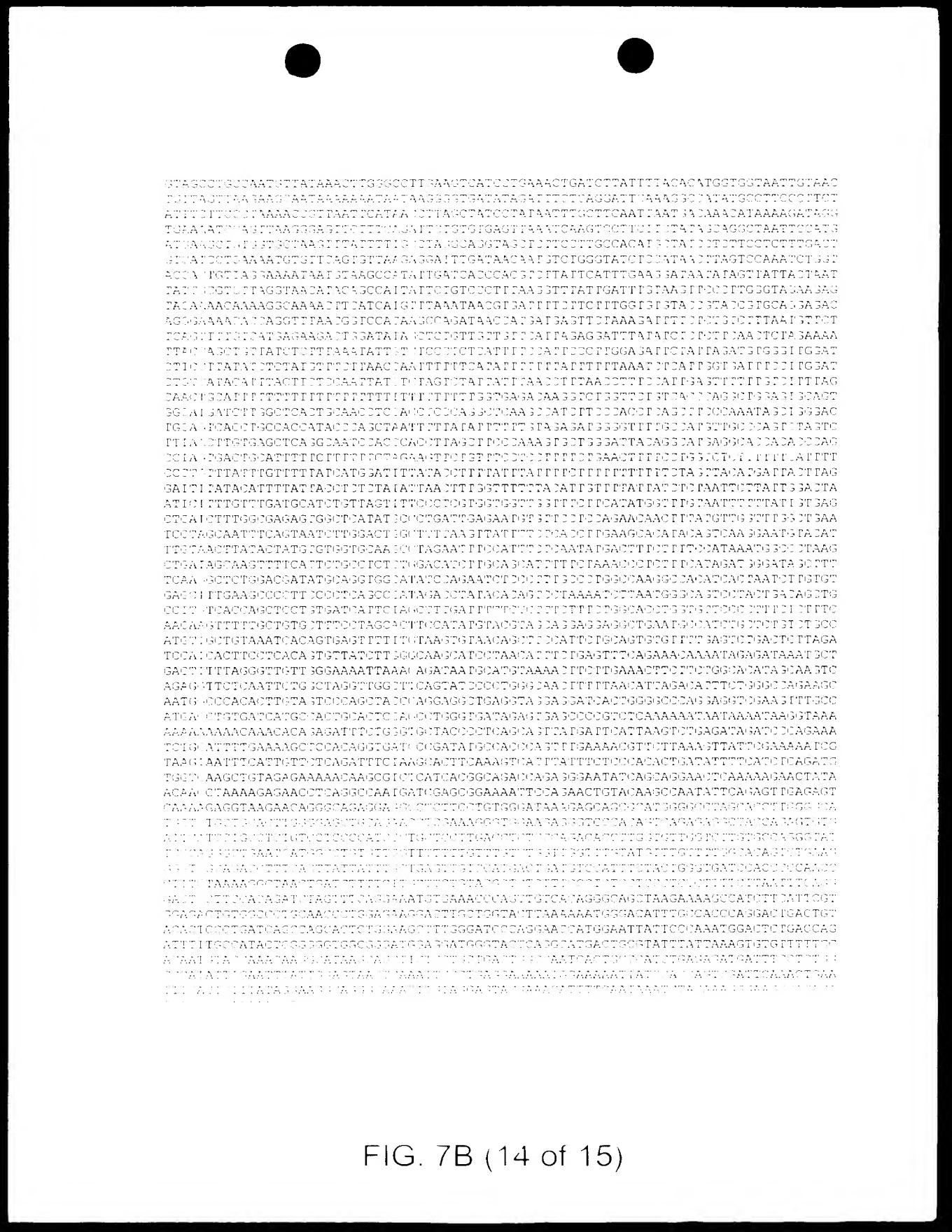


FIG. 7B (14 of 15)

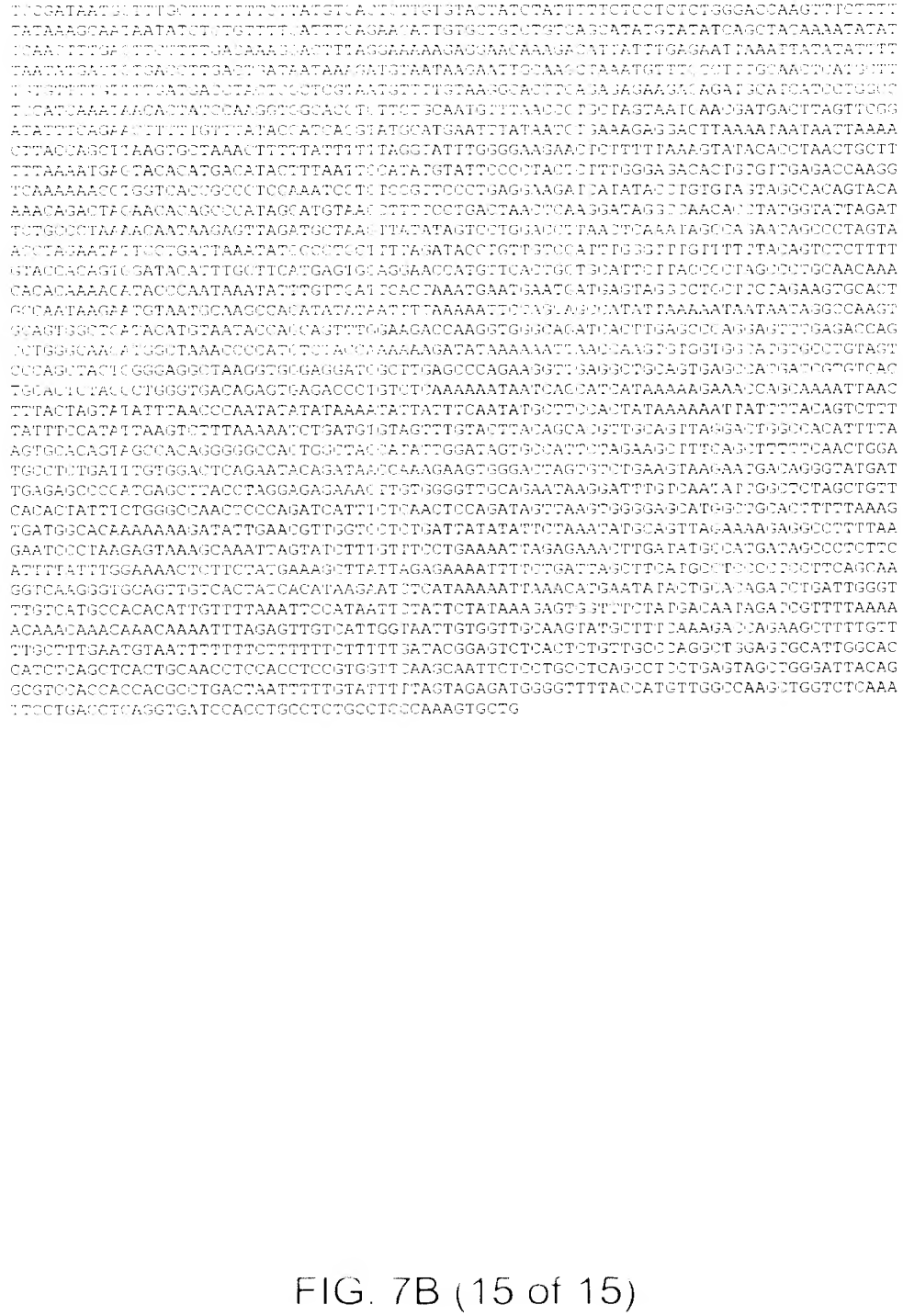


FIG. 7B (15 of 15)

FIG. 7C

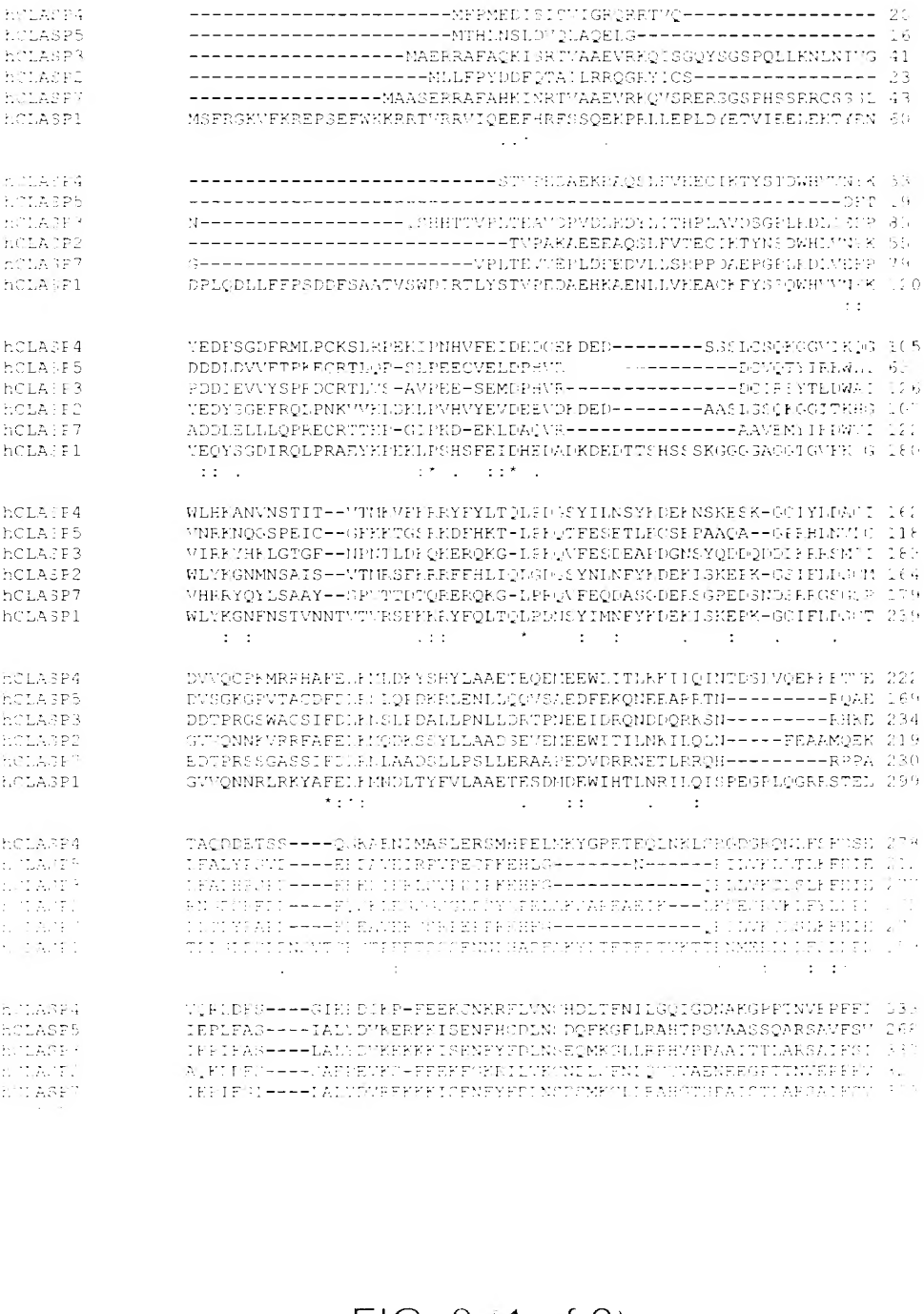


FIG. 8 (1 of 6)

FIG. 8 (2 of 6)

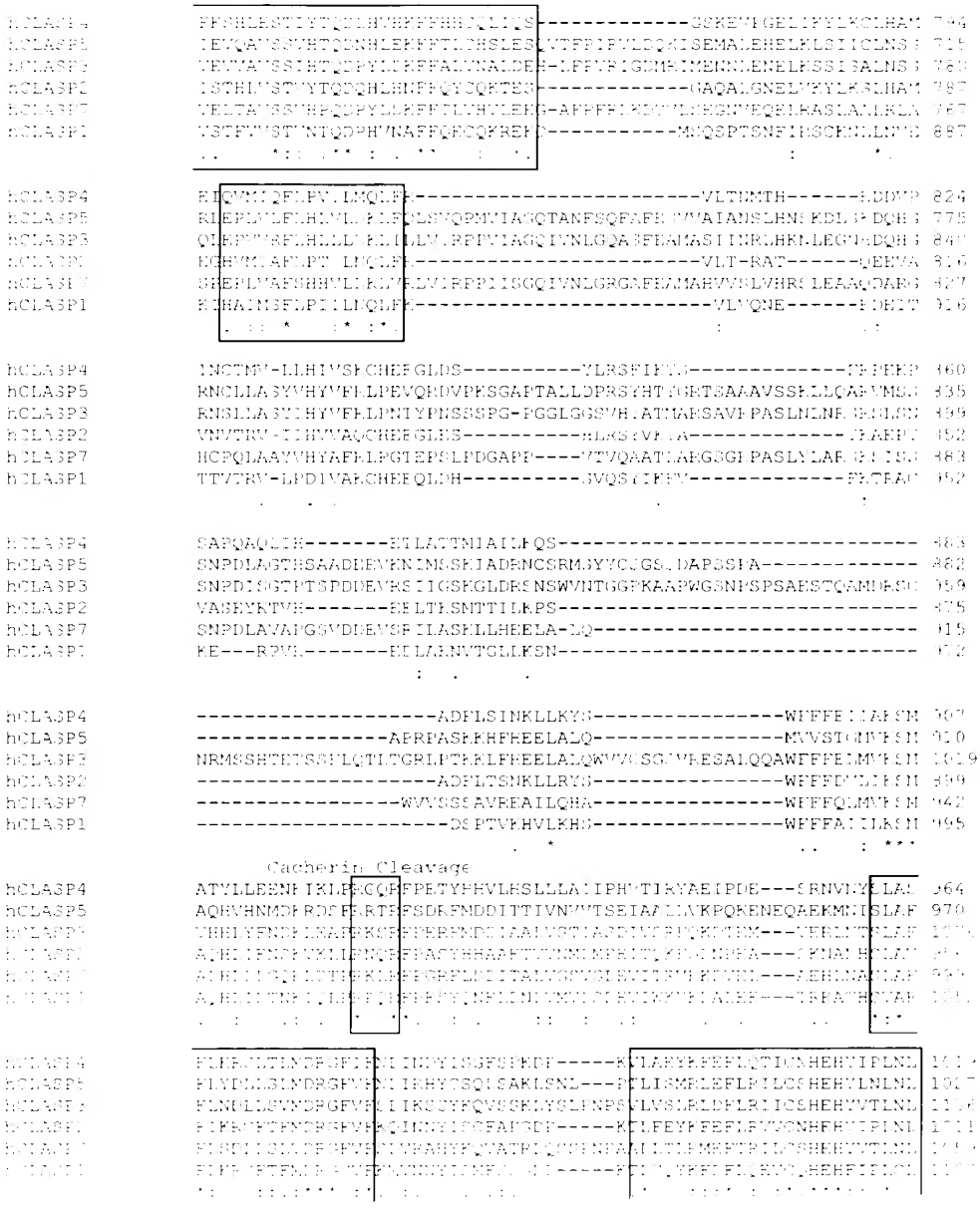


FIG. 8 (3 of 6)

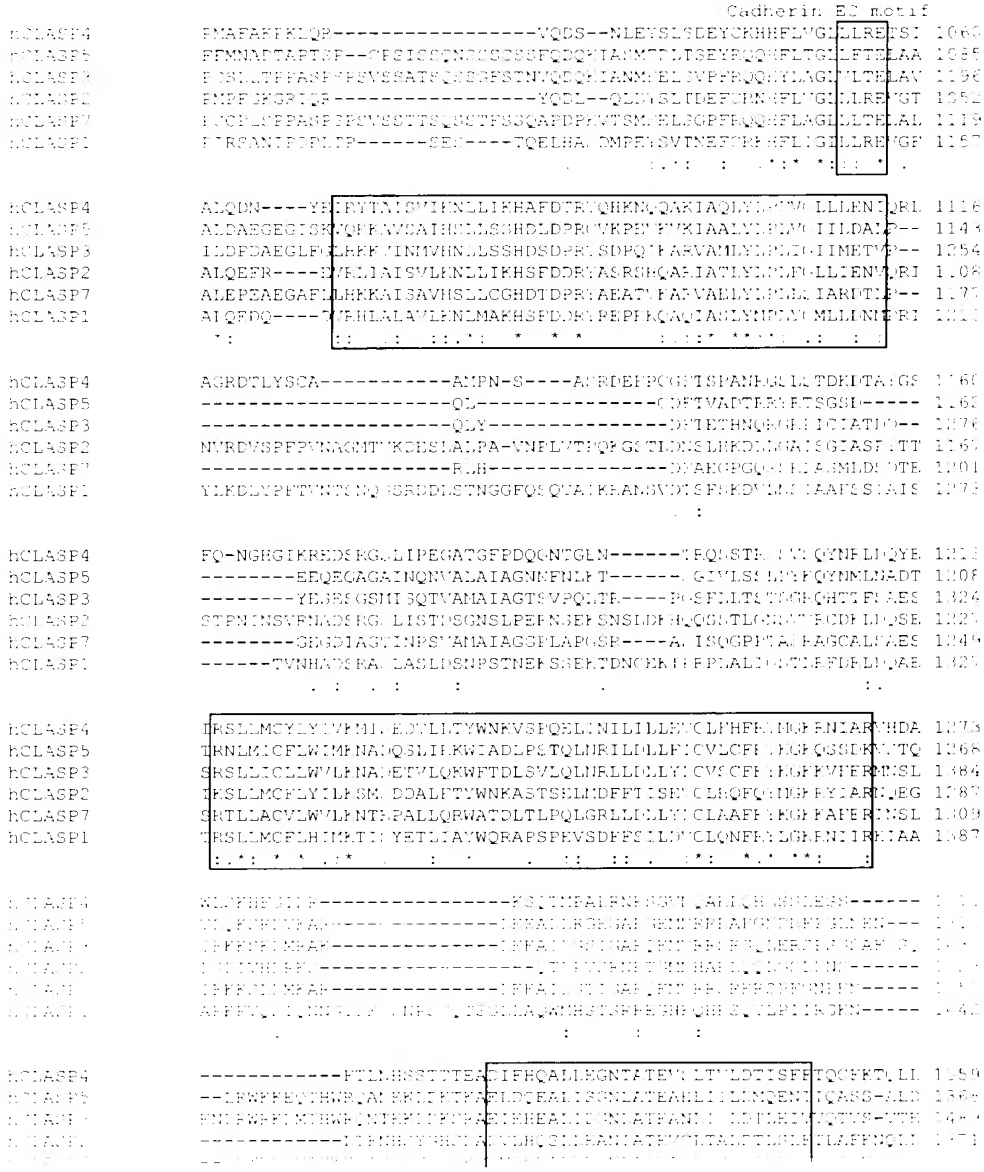


FIG. 8 (4 of 6)

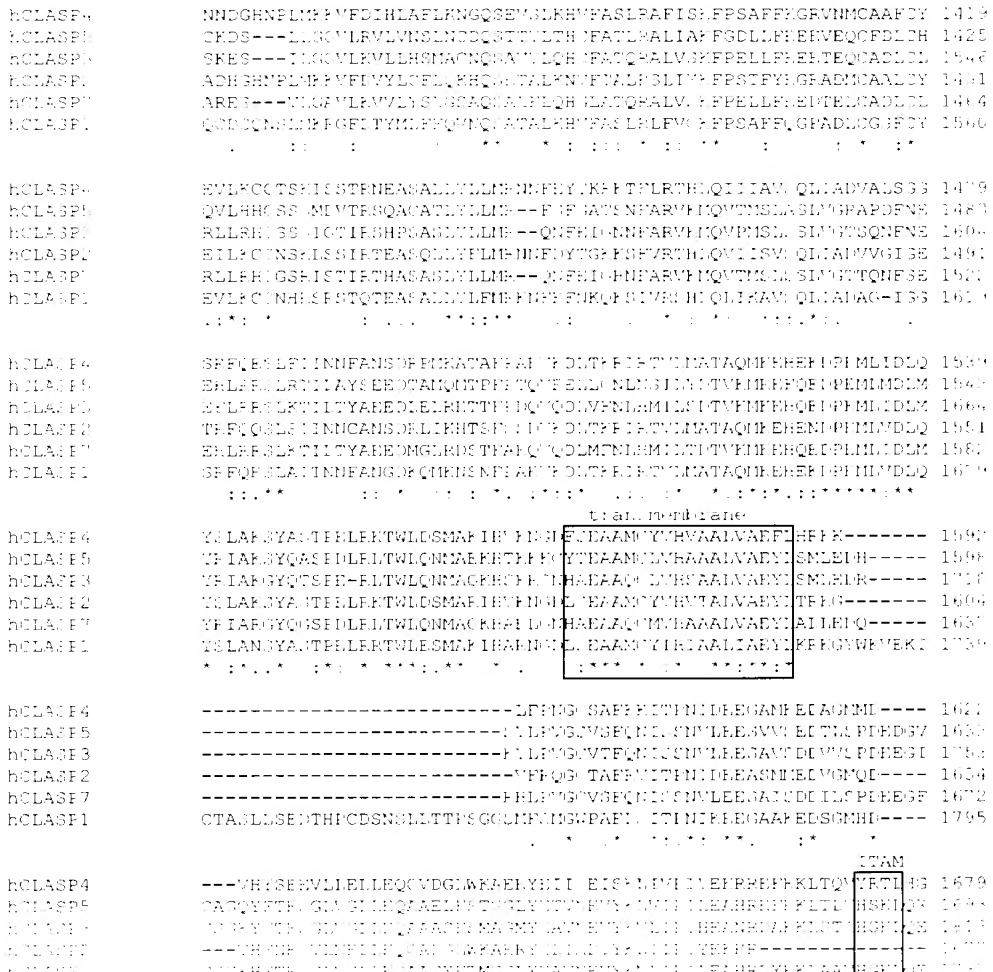

hCLASP4
hCLASP5
hCLASP3
hCLASP2
hCLASP7
hCLASP1
transmembrane
ITAM
ITAM
SOCS motif
DECK motif
ITAM

FIG. 8 (5 of 6)

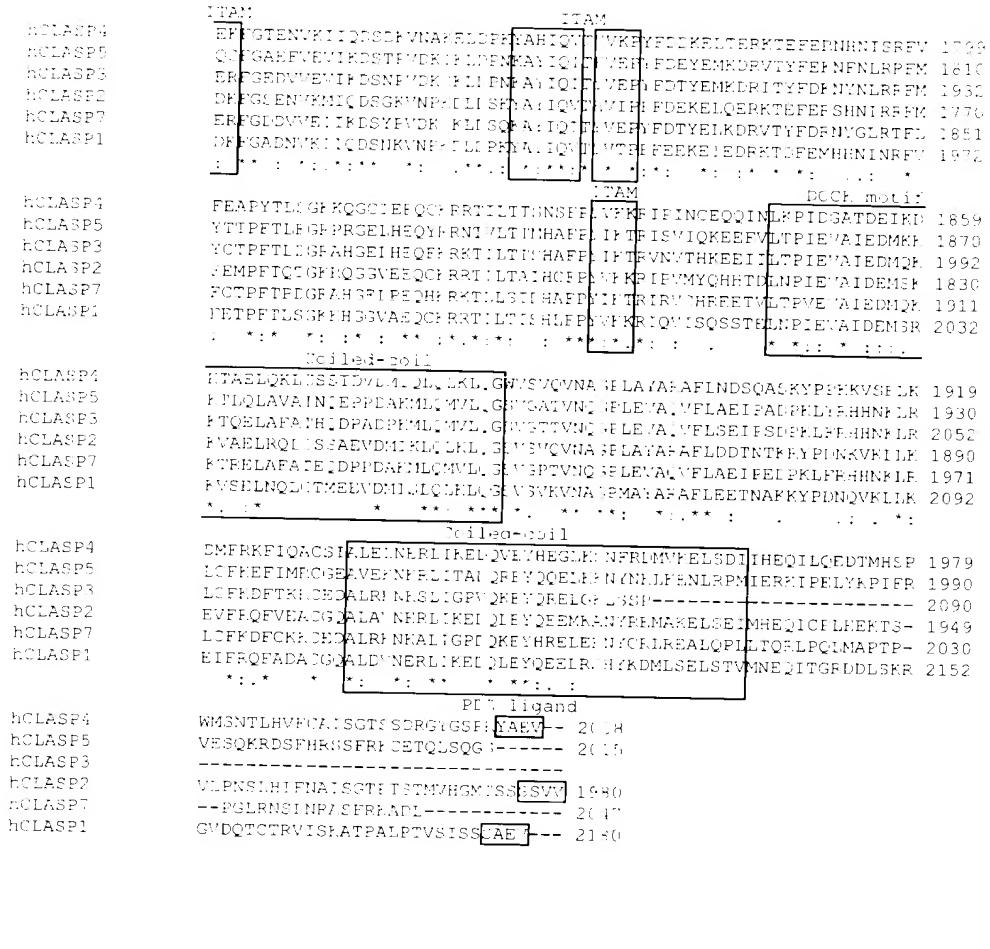

ITAM
ITAM
hCLASP4
hCLASP5
hCLASP3
hCLASP2
hCLASP7
hCLASP1
ITAM
DCCK motif
hCLASP4
hCLASP5
hCLASP3
hCLASP2
hCLASP7
hCLASP1
Coiled-coil
hCLASP4
hCLASP5
hCLASP3
hCLASP2
hCLASP7
hCLASP1
Coiled-coil
hCLASP4
hCLASP5
hCLASP3
hCLASP2
hCLASP7
hCLASP1
PDZ ligand

FIG. 8 (6 of 6)